

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 23, 2005, 08:17:54 ; Search time 23433 Seconds
(without alignments)
17657.111 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
Sequence: 1 CTGACGCGCCCTGTAGCGGC.....atactacacaccaccacct 8539

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb Da: *
2: gb Hcg: *
3: gb In: *
4: gb Om: *
5: gb Ov: *
6: gb Pac: *
7: gb Ph: *
8: gb Pl: *
9: gb Pr: *
10: gb Ro: *
11: gb Str: *
12: gb Sy: *
13: gb Un: *
14: gb Vt: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8539	100.0	11282	6	BD203630 Inducible
2	8539	100.0	11282	6	CQ790428 Sequence
3	8539	100.0	11282	6	AR342585 Sequence
4	8539	100.0	11282	6	AX128601 Sequence
5	8539	100.0	11282	6	AX174827 Sequence
6	7657.2	89.7	13068	6	CQ790429 Sequence
7	7657.2	89.7	13068	6	CQ790448 Sequence
8	7657.2	89.7	17753	6	CQ790449 Sequence
9	7637.4	89.4	9951	6	AR282858 Sequence
10	7637.4	89.4	9951	6	AX128602 Sequence
11	7637.4	89.4	10524	6	AR282859 Sequence
12	7637.4	89.4	11927	6	AR282860 Sequence
13	7637.4	89.4	13905	6	AR137241 Sequence
14	7637.4	89.4	13905	6	AR282856 Sequence
15	7634.8	89.4	8000	6	AR221249 Sequence
16	7634.8	89.4	8000	6	AR230676 Sequence
17	7634.8	89.4	8000	6	AR234150 Sequence
18	7634.8	89.4	8000	6	AR237760 Sequence
19	7634.8	89.4	8000	6	AR353270 Sequence

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21	7634.8	89.4	8000	6	BD085671
22	7634.8	89.4	11703	14	SING
23	7634.8	89.4	11740	6	AR221250
24	7634.8	89.4	11740	6	AR230677
25	7634.8	89.4	11740	6	AR234151
26	7634.8	89.4	11740	6	AR237761
27	7634.8	89.4	11740	6	AR353271
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31	7634.8	89.4	11703	6	AR042412
32	7618.8	89.2	11703	6	AR096558
33	7618.8	89.2	11703	6	AR345324
34	7618.8	89.2	11703	6	AR345324
35	7618.8	89.2	11703	6	BD071123
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37	7617.2	89.2	8000	6	AR230675
38	7617.2	89.2	8000	6	AR234149
39	7617.2	89.2	8000	6	AR237759
40	7617.2	89.2	8000	6	AR353269
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42	7617.2	89.2	8000	6	BD085670
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44	7612.4	89.1	16656	6	AR043384
45	7612.4	89.1	16656	6	AR062299

ALIGNMENTS

RESULT 1	BD203630	11282 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD203630				
DEFINITION	Inducible alpha virus gene expression system.				
ACCESSION	BD203630				
VERSION	BD203630.1	GI:33013400			
KEYWORDS	JP 2002509729-A/1.				
SOURCE	synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	1 (bases 1 to 11282)				
AUTHORS	Renner, W.A., Nieba, L. and Boorsma, M.				
TITLE	Inducible alpha virus gene expression system				
JOURNAL	Patent: JP 2002509729-A 1 02-APR-2002;				
COMMENT	CYTOS BIOTECHNOLOGY AG				
OS	Artificial Sequence				
PN	JP 2002509729-A/1				
PD	02-APR-2002				
PF	25-MAR-1999 JP 2000541320				
PR	27-MAR-1998 US 60/079562				
PI	WOLFGANG A. RENNER, LARS NIEBA, MARCO BOORSMA				
PC	C12N15/09, A01K67/027, A61K48/00, C07K14/18, C12N1/15, C12N1/19, PC				
	C12N1/21,				
	PC C12N5/10, C12N7/04, C12N9/12, C12N15/00, C12N5/00 CC				
	of Artificial Sequence: cDNA				
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FT	source	Location/Qualifiers			
FEATURES	source	Location/Qualifiers			
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	/mol_type="genomic DNA"				
	/db_xref="taxon:32630"				
ORIGIN					
Query Match	100.0%; Score 8539; DB 6; Length 11282;				
Best Local Similarity	100.0%; Pred. No. 0;				
Matches 8539; Conservative	0; Mismatches 0; Indels 0; Gaps 0;				

OR 1 CTGACGCGCCCTGTAGCGGCACATTAGCGCGGGGTGTGTGTTACGCGCAGCGCTGA 60
DB 1 CTGACGCGCCCTGTAGCGGCACATTAGCGCGGGGTGTGTGTTACGCGCAGCGCTGA 60

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Db 61 CCGCTACACTTGGCCAGCGCCCTAGCGCCGCTCTTTCGCTTTTCCTTCCCTTCTTCG 120
QY 121 CCAAGTTCCGCGGGCTTTCCCGCTCAAGCTCTAAATTCGGGGGCTCCCTTAAAGGTTCCGAT 180
Db 121 CCAAGTTCCGCGGGCTTTCCCGCTCAAGCTCTAAATTCGGGGGCTCCCTTAAAGGTTCCGAT 180
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Db 241 GGCATGCGCTGTATGACGCTTTTTCGCTTTTTCGCTTTGAGCTTTCAGCTTCTTTATA 300
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QY 1381 AACATGCGTCCGAATTTTCCGTATGACAGAGCTGTATATCAACGCTCCGGAATATC 1440
Db 1381 AACATGCGTCCGAATTTTCCGTATGACAGAGCTGTATATCAACGCTCCGGAATATC 1440
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Db 1441 TATCATCAGGCTATGAAAGCGGCGGACCCGTATCTGGAATTGGCTTCGACACACCGAG 1500
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QY	4921	CAATTCAACCCCGCACATCTGAATTCGCTGATTCGTCGCTGTAGAGGTACAAAGAT	4980
Db	4921	CAATTCAACCCCGCACATCTGAATTCGCTGATTCGTCGCTGTAGAGGTACAAAGAT	4980
QY	4981	GGAAGTTGAGCCGGCCGTCAATTCGCGACCAAAAGGAGAAATTTGCTGACTGCAAGAG	5040
Db	4981	GGAAGTTGAGCCGGCCGTCAATTCGCGACCAAAAGGAGAAATTTGCTGACTGCAAGAG	5040
QY	5041	GAGAGAGTTGCCAACGCGACCAATCCGCTGGGTGACCCAGGCGAAAGATCTGCGCGTGC	5100
Db	5041	GAGAGAGTTGCCAACGCGACCAATCCGCTGGGTGACCCAGGCGAAAGATCTGCGCGTGC	5100
QY	5101	ATCTATAACGTTGAGCCGACAGGTTTTACGATTCAGGCAAGGACACCGCACG	5160
Db	5101	ATCTATAACGTTGAGCCGACAGGTTTTACGATTCAGGCAAGGACACCGCACG	5160
QY	5161	ATGACTGTGTGCTTACGAAAGAAATGTATCCAGCGCGTCCGCTGATTTCCGAAAGCAC	5220
Db	5161	ATGACTGTGTGCTTACGAAAGAAATGTATCCAGCGCGTCCGCTGATTTCCGAAAGCAC	5220
QY	5221	CCAGAGCAGAGGCGCTTGAATTTGCTCAAAACCGCTTACATATGAGTGGCAGATTATGTA	5280
Db	5221	CCAGAGCAGAGGCGCTTGAATTTGCTCAAAACCGCTTACATATGAGTGGCAGATTATGTA	5280
QY	5281	AATGAACTTAACATCAGAGTCTGTGCGCATTTCCACTGCTATCTACAGCAATTTACGACCC	5340
Db	5281	AATGAACTTAACATCAGAGTCTGTGCGCATTTCCACTGCTATCTACAGCAATTTACGACCC	5340
QY	5341	GGAAGAGCGCGCTTGAAGTATCATTAACCTGTGACCAACCGGCGTACAGAACCTGAC	5400
Db	5341	GGAAGAGCGCGCTTGAAGTATCATTAACCTGTGACCAACCGGCGTACAGAACCTGAC	5400
QY	5401	GCGGACGTAAACCATCTATTTGCTGTGATTAAGAAAGTGAAGAAAGAAATCGACGCGCACCTC	5460
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QY	5581	AAATTTGATTTGCTATCTTGAAAGGCAACCAATTCATCAAGCAGCAAAAAGACATGGCGGAG	5640
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QY	5701	GGTGAGACCATGAGAAAGAAATCCGCGAAAGTGCCTGGTTCGACATAAACCCGCTCTAGC	5760
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QY	5761	CCGCCCAAAACGTTGCCGTGCTTTGCAATGATATGCCATGACCGCAAAAGGGTTCACAGA	5820
Db	5761	CCGCCCAAAACGTTGCCGTGCTTTGCAATGATATGCCATGACCGCAAAAGGGTTCACAGA	5820
QY	5821	CTTAGAAGCAATTAAGTCAAAAGAAATTACAGTATGCTCTCACCCGCTTCTTAAGAC	5880
Db	5821	CTTAGAAGCAATTAAGTCAAAAGAAATTACAGTATGCTCTCTCACCCGCTTCTTAAGAC	5880
QY	5881	AAAAATTAAAGATGTTCAAGAAAGTTCACTGACAGAAAGTACTGTTTAATCCGACACT	5940
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QY	5941	CCCGCATTCGTTCCCGCCCGCTAATGATATGAAATGTCACAAACGCTTACCGCTCTCT	6000
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Db	6001	GCAACAGGCCGAGGAGGCCCCCGGAAGTTGTAGCGCAACCGTCACCATCTACAGCTGATATAC	6060
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QY	6121	TTTTCGAGCTTTAGCGGATCGGACCAACTCTAATTACTGTATGTGACAGTTGGTGGTCAAGA	6180
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QY	6181	CTTAGTTCACTAGAGATAGTAGACCGAAGGCAAGGTGTGTGCTGAAGTTATGCCGCT	6240
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QY	6361	GGGGTATTCATATGTCCTTCGGAATCAATTTTGAAGGAAGACGCGCCCAAGGACGCGTA	6420
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QY	6421	CAACCCCTGCAACAGGCCCCCAAGATGTGCTATGCTTTGGATGTTTTCGACGGA	6480
Db	6421	CAACCCCTGCAACAGGCCCCCAAGATGTGCTATGCTTTGGATGTTTTCGACGGA	6480
QY	6481	GAGATTGATAGCTGAGCCGCAAGTAATCTGAGTCCGAAACCCGTCGTTGGATCAATTT	6540
Db	6481	GAGATTGATAGCTGAGCCGCAAGTAATCTGAGTCCGAAACCCGTCGTTGGATCAATTT	6540
QY	6541	GAACCGGGCGAAGTAATTAATATGCTCCGATCAACCCGATCTTTTTCACATACGC	6600
Db	6541	GAACCGGGCGAAGTAATTAATATGCTCCGATCAACCCGATCTTTTTCACATACGC	6600
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ORIGIN
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QY	61	CCGCTACACTTGGCCAGCGCCCTAGCGCGCGCTCTTTGGCTTTCTTCCTCTCTCTCTCG	120
Dp	61	CCGCTACACTTGGCCAGCGCCCTAGCGCGCGCTCTTTGGCTTTCTTCCTCTCTCTCTCG	120
QY	121	CCAGGTTGGCGGCTTTTCCCGGTCAAGCTCTAAATCGGAGGCTCCCTTTAGGGTTCCGAT	180
Dp	121	CCAGGTTGGCGGCTTTTCCCGGTCAAGCTCTAAATCGGAGGCTCCCTTTAGGGTTCCGAT	180
QY	181	TTAGGCTTTACGCGACCTCGACCCCAAAAAAATTGATTTAGGGTATGTTACGTATG	240
Dp	181	TTAGGCTTTACGCGACCTCGACCCCAAAAAAATTGATTTAGGGTATGTTACGTATG	240
QY	241	GGCCATCGCCCTGATGACGGTTTTTGGCCCTTTGAGCGTTGGAGTCCACGTTCTTTAATA	300
Dp	241	GGCCATCGCCCTGATGACGGTTTTTGGCCCTTTGAGCGTTGGAGTCCACGTTCTTTAATA	300
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Dp	301	GTGACCTGTTGTTCCAAACTGSAACAACACTCAACCTCATCTCGGTCTAATCTTTGAT	360
QY	361	TATAAGGATTTTGGCGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTAACAAAAAT	420
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Dp	421	TTAAACGCAATTTTAAACAAATATTAAAGCTTAACAATTTCCATTGCGATTCAAGCTCG	480
QY	481	CAACTGTTGGGAAGGCGATCGTGGCGGCTCTCGCTATTACGCGACGTGGCCGAAG	540
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QY	601	TAAACGACGCGCAGTGAAGCGCGCAATTAACCCCTCACTAAAGGGGAACAAAGCTGGAG	660
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Dp	721	CATGCCCTTACAAAGAGAAAGAACCGGTGCATGCGGCTTGGTGAAGTAAAGTGGTAC	780
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QY	1081	GCATTTTCGCATCTGGCCAGTAACTATACGAGCTGGAGGTTCTCTTACACAGCACGATC	1140
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QY	1141	TTGACATAGGCACGCGCACCGGCTCGTATGAAATGTTTTCCGAGCACAGTATCATTTGTCTC	1200
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Db	1261	GA AAAAGCGTSCAAGATTACAAACAGAATTGTCATGAGAAAGATTAAAGATCTCCGAGCC	1320
QY	1321	GTA CTCTGATAGCCGGAGTCTGTAACACATCCGCTTCGCTTTCAACATGATTAACCTGC	1380
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RESULT 3
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DEFINITION Sequence 1 from patent US 6576443.
ACCESSION AR342585
VERSION AR342585.1 GI:33737767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11282)
AUTHORS Hennecke, F. and Remner, W.A.
TITLE Replicon based activation of endogenous genes
JOURNAL Patent: US 6576443-A 1 10-JUN-2003;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 781 GATCGTCTTATTTAGGAAGCAACGAGGCTGACATGATTTGAGTGAAGCAACCTGAA 840
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DB 841 TTCCGATTCAGAGATATTTGATTTAAGTGCCTTTCGCTTTCGCTTTCGCTTTCGCTTTCGCT 900
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DB 901 CGTAGACACACTATTTGAATCAACAGCGCAATTTGACATTCATCAATGAGAG 960
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DB 1021 TTCCCGCAATTTGAGTATGACAGACGCTCTCAATATGACATCTAATGCGAGA 1080
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DB 1081 GCAATTTTGCATCTGCGCAATTAATCGAGTGGAGTTCTTTCGCAACGACGAGATC 1140
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DB 1141 TTGACATATGAGAGGCAACCGCTCTGTAAGATTTTTCGAGACCAAGATATCTGTGTC 1200
QY 1201 TCCCCCATGCTGATGTCAGAGACCCGCAACCGCATGATGAAATACGCACTGAACTGAGG 1260
DB 1201 TCCCCCATGCTGATGTCAGAGACCCGCAACCGCATGATGAAATACGCACTGAACTGAGG 1260
QY 1261 GAAAAAGCTGCAAGATTAACAAACAACTTGCATGAGAAATTAAGATCTCCGAGAC 1320


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Db 1441 TATATCAGGCTATGAAAAGGCTGCGACCTGTACTGTGATTTGGCTTTCAGACCAACCAG 1500
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Db	5701	GGTGAAGCATGGAAGCAATCCGGGAAAAGTCCCGGTGACATTAACCCGTCGTACAGC	5760
Qy	5761	CCGCCCAAAACGTTGCGGTGCTTTCATGTATGCGATGACGCGGAAGGGTCCACAGA	5820
Db	5761	CCGCCCAAAACGTTGCGGTGCTTTCATGTATGCGATGACGCGGAAGGGTCCACAGA	5820
Qy	5821	CTTGAAGCATPAACGTGAAGAAAGTTACATATGCTCTCCACCCCTTCCTAAGAC	5880
Db	5821	CTTGAAGCATPAACGTGAAGAAAGTTACATATGCTCTCCACCCCTTCCTAAGAC	5880
Qy	5881	AAAAATTAAAGATGTTCAGAAAGTTCAAGTCAAGAAAGTACCTGTTTAATCCGACACT	5940
Db	5881	AAAAATTAAAGATGTTCAGAAAGTTCAAGTCAAGAAAGTACCTGTTTAATCCGACACT	5940
Qy	5941	CCCGCATTCGTTCCCGCCCGTAAAGTACATAGAAGTCCAGAAAGCCTACCGCTCTCT	6000
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Qy	6001	GCAACAGCGCGAAGAGGCCCCCGGAAGTTGTACGACACCGTCAACATCTACAGCTGATAC	6060
Db	6001	GCAACAGCGCGAAGAGGCCCCCGGAAGTTGTACGACACCGTCAACATCTACAGCTGATAC	6060
Qy	6061	ACCTGCGTTGAATGTCACAGACATCTCACTGATATGATGACAGTAGGCGAAGGCTCACTT	6120
Db	6061	ACCTGCGTTGAATGTCACAGACATCTCACTGATATGATGACAGTAGGCGAAGGCTCACTT	6120
Qy	6121	TTTTGAGACTTTAAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGTCGTACAGA	6180
Db	6121	TTTTGAGACTTTAAGCGGATCGGACAACTCTATTACTAGTATGACAGTTGGTCGTACAGA	6180
Qy	6181	CCTAGTCACTAGAGATAGTAGACCGAAGGCGAGTGTGTGTGCTGACAGTTCAATGCCGT	6240
Db	6181	CCTAGTCACTAGAGATAGTAGACCGAAGGCGAGTGTGTGTGCTGACAGTTCAATGCCGT	6240
Qy	6241	CAAGAGCGTGGCCCCCTAATCCACCGCGCAAGGCGTAAAGAAAGATGGCCCCGTCGACGCGCA	6300
Db	6241	CAAGAGCGTGGCCCCCTAATCCACCGCGCAAGGCGTAAAGAAAGATGGCCCCGTCGACGCGCA	6300
Qy	6301	AGAAAAGAGCCCACTCCACCGCGCAAGCAATAGCTGAGTCCCTCCACTCTCTTTTGGT	6360
Db	6301	AGAAAAGAGCCCACTCCACCGCGCAAGCAATAGCTGAGTCCCTCCACTCTCTTTTGGT	6360
Qy	6361	GGGGTATCCATGTCCCTCGGATCAATTTTTCGACGAGAGACGGCCCGCAAGGACGGTAA	6420
Db	6361	GGGGTATCCATGTCCCTCGGATCAATTTTTCGACGAGAGACGGCCCGCAAGGACGGTAA	6420
Qy	6421	CAACCCCTGGCAACAGGCGCCACGGATGTCCTAATGCTTTTCGATCGTTTTCGACGGA	6480
Db	6421	CAACCCCTGGCAACAGGCGCCACGGATGTCCTAATGCTTTTCGATCGTTTTCGACGGA	6480
Qy	6481	GAGATTGATGAGCTAGCGCGACAGATTACTGAGTCCGAACCCGTCCTGTGGATCATTT	6540
Db	6481	GAGATTGATGAGCTAGCGCGACAGATTACTGAGTCCGAACCCGTCCTGTGGATCATTT	6540
Qy	6541	GAACCGGCGGAAGTGAATCTAATTATCGTCCGATCAGCCGATCTTTTCCACTACGC	6600
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Db	6601	AAGCAGAGACGTAGACGACGAGGACGAGAGATGATCTGATCTAAACGGGGGTAGTGGG	6660
Qy	6661	TACATATTTTTCGACGAGACAGAGCCCTGGGCACTTGCAGAAAGAAAGTCCGTTCTGCAAGAC	6720
Db	6661	TACATATTTTTCGACGAGACAGAGCCCTGGGCACTTGCAGAAAGAAAGTCCGTTCTGCAAGAC	6720
Qy	6721	CAGCTTACAGAACCGACCTTGGAGGCGCAATGTCCTGAAAGAAATTCATGCCCGGTGCTC	6780

D	6721	CAGCTTACGAAACCGACCTTGGAGCCGGAATGTCTCGAAAGAAATTCAATGCCCGGTCTC	6780
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D	6781	GACACGTCGAAAAGAGAACTCAACTCAACTCAGTACCAAGATGATGCCACCGAAGCCAC	6840
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D	6841	AAAAGTGGTACCAAGTCTCTCGTAAAGTGAAGAAATAGAAAGCAATACCACTGAGCGCTA	6900
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D	6901	CTGTACAGACTACGACTGTATTAATCTCTGCCACATCAGCCAGCAATCTATTAAGTACCC	6960
Q	6961	TATCCGAAACCATTTGTACTCCAGTAGCGGTACCGGCGAACTATCTCGATTCACAGTTGCT	7020
D	6961	TATCCGAAACCATTTGTACTCCAGTAGCGGTACCGGCGAACTATCTCGATTCACAGTTGCT	7020
Q	7021	GTAGCTGTCTGTAACTAACTATCTGCAATGAGAACTATCCGACAGTAGCATCTTATCAAT	7080
D	7021	GTAGCTGTCTGTAACTAACTATCTGCAATGAGAACTATCCGACAGTAGCATCTTATCAAT	7080
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D	7081	ACTGACAGTAGTACAGTGGCTTACTTGGAATATGGTAAACGACAGTCGCGATGCTGATACT	7140
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D	7141	GCAACCTTCTTGCTCCCGCTTAAGCTTAAAGATTACCCGAAAAACATAGATATAGACCCCG	7200
Q	7201	AATATCCGCAATGGGCTTCCATCAGCGATGCAAAACAGCTTACAAATATGTCTCATTTGCC	7260
D	7201	AATATCCGCAATGGGCTTCCATCAGCGATGCAAAACAGCTTACAAATATGTCTCATTTGCC	7260
Q	7261	GCAACTAAAGAAATTTGCAAGCTACGCAATGGGTGAACCTGCCAACCTGGAATCAGCG	7320
D	7261	GCAACTAAAGAAATTTGCAAGCTACGCAATGGGTGAACCTGCCAACCTGGAATCAGCG	7320
Q	7321	ACATTCAATGTTCGATGCTTTCGAAAATATGATCATGTATGACAGATATTTGGAGAGATTC	7380
D	7321	ACATTCAATGTTCGATGCTTTCGAAAATATGATCATGTATGACAGATATTTGGAGAGATTC	7380
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D	7381	GCTCGGAAGCCAAATTAAGATTACCACTGAGTTTGTCAACCGCATATGTAGCTAGCTGAAA	7440
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D	7441	GGCCTTAAGGCGCGCGCACTATTTTGCAAAAGCGATATAATTTTGTCCTCATTTGCCAAGAGTG	7500
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D	7501	CTTATGATTAAGTTCGTATGATGACATGTAAGAAAGACGTAAGAAAGTTTACACAGGACGAAA	7560
Q	7561	CACAAGAAAGAACCCGAAAGTACAAAGTATACAAAGCCGCGAAGCCCTTGCGACTGCT	7620
D	7561	CACAAGAAAGAACCCGAAAGTACAAAGTATACAAAGCCGCGAAGCCCTTGCGACTGCT	7620
Q	7621	TACTTATGCGGGATTCACCGGGAATTAAGTGGTATGAGCTTACGCGCTTCTTCCAAAC	7680
D	7621	TACTTATGCGGGATTCACCGGGAATTAAGTGGTATGAGCTTACGCGCTTCTTCCAAAC	7680
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VERSION CO790429.1 GI:45823471
KEYWORDS
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REFERENCE
1 Ivanova, L., Renner, W.A. and Saudan, P.
Inducible alphaviral/orf1 based gene expression system
Patent: WO 2004018506-A 2 04-MAR-2004;
JOURNAL Cytos Biotechnology AG (CH)
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Source Location/Qualifiers

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ORIGIN

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Db	5309	ACGCAAGCCGAGAAAAGACCGGCTTTGAAGTATCACTTAACTGTGTGACAAACCGCGCTAGACA	5368
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Db	6209	ATGCCGTCCAAAGAGCTGCCCCCTATTTCCACCGCAAGGCTTAAGAAAGATGGCCCGCTGG	6268
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Qy	6593	CACCTACCGAAGCAGAGAGCTAGACGACAGAGCAGAGAGACTGAATCTGACTAAACCGGGG	6652
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VERSION CQ790448.1 GI:45823490
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SOURCE
ORGANISM
REFERENCE 1
AUTHORS Ivanova, L., Renner, W. A. and Saudan, P.
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Cytos Biotechnology AG (CH)
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ORIGIN
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QY 5933 CGCAACTCCCGCATTCGTTCCCGCCGTAAGTACATTAAGATGCGCAAAACGCTTACG 5992
Db 5909 CGCAACTCCCGCATTCGTTCCCGCCGTAAGTACATTAAGATGCGCAAAACGCTTACG 5968
QY 5993 CTCCTCTGACAGGCGGAGAGGCGCCCGAAAGTTGTACGACACCGTCAACATCAACG 6052
Db 5969 CTCCTCTGACAGGCGGAGAGGCGCCCGAAAGTTGTACGACACCGTCAACATCAACG 6028
QY 6053 CTGATTAACACTCGCTTGAATGTCACAGACATCTCATGATATGATGAAGTAGAGGAAG 6112
Db 6029 CTGATTAACACTCGCTTGAATGTCACAGACATCTCATGATATGATGAAGTAGAGGAAG 6088
QY 6113 GCTCACTTTTTCGAGCTTTTACGCGATCGGACAACTCTATTACTAGTATGACAGTTGGT 6172
Db 6089 GCTCACTTTTTCGAGCTTTTACGCGATCGGACAACTCTATTACTAGTATGACAGTTGGT 6148
QY 6173 CGTCAAGGACCTAGTTCATAGAGATTAAGTACCGAAGGAGGAGTGGTGGCTGACGTTCC 6232
Db 6149 CGTCAAGGACCTAGTTCATAGAGATTAAGTACCGAAGGAGGAGTGGTGGCTGACGTTCC 6208
QY 6233 ATGCGGTCCAAGACCTGCGCTTATTCACCGCCAAAGCTAAAGAAAGATGGCCCGCTGG 6292
Db 6209 ATGCGGTCCAAGACCTGCGCTTATTCACCGCCAAAGCTAAAGAAAGATGGCCCGCTGG 6268
QY 6293 CAGCGGCAAGAAAGAAAGCCCACTCCACCGGCAAGCAATAGCTGTAGTCCCTCCACTCT 6352
Db 6269 CAGCGGCAAGAAAGAAAGCCCACTCCACCGGCAAGCAATAGCTGTAGTCCCTCCACTCT 6328
QY 6353 CTTTGTGGGGTATCCATGTCCTCGATCAATTTTTCAGACGAGAGAGCGGCCGCGACG 6412
Db 6329 CTTTGTGGGGTATCCATGTCCTCGATCAATTTTTCAGACGAGAGAGCGGCCGCGACG 6388
QY 6413 CAGCGGTACACCCCTGCGCAACGAGCCCAAGATGTGCTGATCTTTTGGATGCTTTT 6472
Db 6389 CAGCGGTACACCCCTGCGCAACGAGCCCAAGATGTGCTGATCTTTTGGATGCTTTT 6448
QY 6473 CCGAGGAGAGATTAATGATGCTGAGCCCGAGTAACTGAATGCCAAACCCGTCCTTTG 6532
Db 6449 CCGAGGAGAGATTAATGATGCTGAGCCCGAGTAACTGAATGCCAAACCCGTCCTTTG 6508
QY 6533 GATCAATTTGAAACCGGCGCAAGTGAATCAATTAATTCGCTCCGATCAGCCGATCTTTTC 6592
Db 6509 GATCAATTTGAAACCGGCGCAAGTGAATCAATTAATTCGCTCCGATCAGCCGATCTTTTC 6568
QY 6593 CACTACGCAAGCAAGACGTAGACCGAGAGGACGAGAGACTGAATTACTGACTTAACCGGG 6652
Db 6569 CACTACGCAAGCAAGACGTAGACCGAGAGGACGAGAGACTGAATTACTGACTTAACCGGG 6628
QY 6653 TAGGTGGGTACATATTTTGCAGCGACAGGCGCTGGGCACTTGAAGAAAGTCCGTTTC 6712
Db 6629 TAGGTGGGTACATATTTTGCAGCGACAGGCGCTGGGCACTTGAAGAAAGTCCGTTTC 6688
QY 6713 TGCAGAACCAAGCTTACAGAACCGACCTTGAAGCGCAATGCTCTGAAAGAAATTCATGCCC 6772
Db 6689 TGCAGAACCAAGCTTACAGAACCGACCTTGAAGCGCAATGCTCTGAAAGAAATTCATGCCC 6748
QY 6773 CCGTGTCTGACACGTCGAAAGAGAAACAATCAAACTAGATTAACAGATGATGCCACCG 6832
Db 6749 CCGTGTCTGACACGTCGAAAGAGAAACAATCAAACTAGATTAACAGATGATGCCACCG 6808
QY 6833 AAGCCAAACAAAAGTATGTAACCAAGTCTGTAAGTGAAGAAATCAGAAAGCATTAACACTG 6892
Db 6809 AAGCCAAACAAAAGTATGTAACCAAGTCTGTAAGTGAAGAAATCAGAAAGCATTAACACTG 6868
QY 6893 AAGCACTACTGTCAAGACTAAGCTGTATTAATCTTCCACAGATGACGCAAGTACTATA 6952
Db 6869 AAGCACTACTGTCAAGACTAAGCTGTATTAATCTTCCACAGATGACGCAAGTACTATA 6928
QY 6953 AGATCACTATCCGAACCAATTTGATCTCAAGTACGCGGCAACTATCTCGATCCAC 7012

Db	6929	AGATCACTTATCCGAACCAATTGTACTCAGTAGCTACCGCGCACTTACCTCGATTCAC	69888
Qy	7013	AGTTGCTGTAGCTGTCTGTAAACAATACTTTCGATGAGAACTATCCGACAGTAGCATCTT	70727
Db	6989	AGTTGCGTGTAGCTGTCTGTAAACAATACTTTCGATGAGAACTATCCGACAGTAGCATCTT	70488
Qy	7073	ATCAGATTACTGACGAGTAGTCAGTCTTATCTTGATATGTGTAGACGAGCAGTCGCATGCC	71322
Db	7049	ATCAGATTACTGACGAGTAGTCAGTCTTATCTTGATATGTGTAGACGAGCAGTCGCATGCC	71089
Qy	7133	TGSAATACTGCAACCTTCTGCCCCGTAGCTTGAAGTTACCCGAAAAAATAGATGATTA	71922
Db	7109	TGSAATACTGCAACCTTCTGCCCCGTAGCTTGAAGTTACCCGAAAAAATAGATGATTA	71688
Qy	7193	GAGCCCCGAAATATCCGACATGCGGTGTCCATAGACGATCGAACAACGCTTACMAAATGTC	72522
Db	7169	GAGCCCCGAAATATCCGACATGCGGTGTCCATAGACGATCGAACAACGCTTACMAAATGTC	72288
Qy	7253	TCATTTGCCGCACTTAAAGAAATTGCAACGTACGCGAGATGCTGMACTCCGCAACATCG	73122
Db	7229	TCATTTGCCGCACTTAAAGAAATTGCAACGTACGCGAGATGCTGMACTCCGCAACATCG	72888
Qy	7313	ACTAGCGCAATTTCAATGTCCAAATGCTTTCCAAAATATGCAATGTAAATGACAGATTTGG	73727
Db	7289	ACTAGCGCAATTTCAATGTCCAAATGCTTTCCAAAATATGCAATGTAAATGACAGATTTGG	73488
Qy	7373	AGGAGTTGCTCGSAAAGCCAAATTAGATTTAACACTGAGATTTTGTCACCGCATATGTAGCTA	74322
Db	7349	AGGAGTTGCTCGSAAAGCCAAATTAGATTTAACACTGAGATTTTGTCACCGCATATGTAGCTA	74088
Qy	7433	GACTGAAAGCCCTTAAGCCCGCCGCACTATTTCGAAAGACGTATTAATTTGGTCCCATTGC	74922
Db	7409	GACTGAAAGCCCTTAAGCCCGCCGCACTATTTCGAAAGACGTATTAATTTGGTCCCATTGC	74688
Qy	7493	AAGAAGTCCCTATGATATGATTTCTGTATGGAATATGAAAGAGACGTGAAAGTTATACCAAG	75533
Db	7469	AAGAAGTCCCTATGATATGATTTCTGTATGGAATATGAAAGAGACGTGAAAGTTATACCAAG	75288
Qy	7553	GCACGAAACACACAGAAAGAACCCGAAAGTACAGTATACAAACGCGACGAAACCCCTGG	76122
Db	7529	GCACGAAACACACAGAAAGAACCCGAAAGTACAGTATACAAACGCGACGAAACCCCTGG	75888
Qy	7613	CGACTGCTTACTTATGCGGGAATTCAACGCGGAATTAGTCGTAGGCTTACCGCCGTCTTGC	76727
Db	7589	CGACTGCTTACTTATGCGGGAATTCAACGCGGAATTAGTCGTAGGCTTACCGCCGTCTTGC	76488
Qy	7673	TTCCAAACATTCAACGCTTTTGTACATGTGCGCGGAGATTTTGTATGCATCATAGCAG	77322
Db	7649	TTCCAAACATTCAACGCTTTTGTACATGTGCGCGGAGATTTTGTATGCATCATAGCAG	77088
Qy	7733	AACACTTCAAGCAAGCGACCCGGAATCTGGAAGACGGAATATGSCATCATTTGCAAAAACC	77922
Db	7709	AACACTTCAAGCAAGCGACCCGGAATCTGGAAGACGGAATATGSCATCATTTGCAAAAACC	77688
Qy	7793	AAGACGACGCTATGCGCTTAAACCGGTCTGATGATTTTGGAGGACCTGCGGTGTGATCAAC	78522
Db	7769	AAGACGACGCTATGCGCTTAAACCGGTCTGATGATTTTGGAGGACCTGCGGTGTGATCAAC	78288
Qy	7853	CACCTACTGCACTTGTATCGAGTGCCTTTGGAGAAATATCATCCACCATCTACCTACGG	79122
Db	7829	CACCTACTGCACTTGTATCGAGTGCCTTTGGAGAAATATCATCCACCATCTACCTACGG	78888
Qy	7913	GTACTCGTTTTAAATTGCGGGGAGATGAGAAATCCGGAATGTTCTCAACATTTTGTGCA	79727
Db	7889	GTACTCGTTTTAAATTGCGGGGAGATGAGAAATCCGGAATGTTCTCAACATTTTGTGCA	79488
Qy	7973	ACACAGTTTGAATGTCTTATTCGCGACAGACAGTACTAGAGAGCGGCTTAAACGTCAC	80322
Db	7949	ACACAGTTTGAATGTCTTATTCGCGACAGACAGTACTAGAGAGCGGCTTAAACGTCAC	80088
Qy	8033	GATGTGACGCGTTCAATGGCGACGACAAATCATATCATGAGTAGTATCTGCAAAAGAA	80922

[illegible]

QY 1073 ATGCCAAGACATTTTCCGATCTGCGCCAGTAACTTAATCGAGCTGGAGGTTCTTACCAAG 1132
DB 1049 ATGCCAAGACATTTTCCGATCTGCGCCAGTAACTTAATCGAGCTGGAGGTTCTTACCAAG 1108
QY 1133 CGAGCATCTTGGACATATGCGCGCCACCGGCTCGTAAGTCTTCCGAGACCAAGATC 1192
DB 1109 CGAGCATCTTGGACATATGCGCGCCACCGGCTCGTAAGTCTTCCGAGACCAAGATC 1168
QY 1193 ATTTGCTGCCCCCATCGTAGTCAGAAAGACCCGACCCGATGATGAATACCCAGTA 1252
DB 1169 ATTTGCTGCCCCCATCGTAGTCAGAAAGACCCGACCCGATGATGAATATTCAGTA 1228
QY 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAAGAACTTGATGAGAAGATTAGATC 1312
DB 1229 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAAGAACTTGATGAGAAGATTAGATC 1288
QY 1313 TCCGGACCGTACTGATATCGCGGATGTGAAACACATCGCTGCTTTCACAAAGATG 1372
DB 1289 TCCGGACCGTACTGATATCGCGGATGTGAAACACATCGCTGCTTTCACAAAGATG 1348
QY 1373 TTACCTGCAACATCGTGCAGATATTTCCGTCATGCAAGACGTTATATCAACGCTCCG 1432
DB 1349 TTACCTGCAACATCGTGCAGATATTTCCGTCATGCAAGACGTTATATCAACGCTCCG 1408
QY 1433 GAATCTATCTATCATCAGGCTATGAAAGCGTGCAGACCTCTGTACTGGAATTGGCTTGCACA 1492
DB 1409 GAATCTATCTATCATCAGGCTATGAAAGCGTGCAGACCTCTGTACTGGAATTGGCTTGCACA 1468
QY 1493 CCACCCAGTTTCATGTTCTCGGCTATGGAGGTTGTGTAACCTCGGCTTACAAACCAACGAGG 1552
DB 1469 CCACCCAGTTTCATGTTCTCGGCTATGGAGGTTGTGTAACCTCGGCTTACAAACCAACGAGG 1528
QY 1553 CCGACGAGAAAGTCTTGAAAGCGGCTAACATCGGACTTTTGACAGCAAAAGCTGAGTAG 1612
DB 1529 CCGACGAGAAAGTCTTGAAAGCGGCTAACATCGGACTTTTGACAGCAAAAGCTGAGTAG 1588
QY 1613 GTAGGACAGGAAATTTGTCATATGAGAGAAAGAGTTGAAGCCCGGCTCGCGGTTT 1672
DB 1589 GTAGGACAGGAAATTTGTCATATGAGAGAAAGAGTTGAAGCCCGGCTCGCGGTTT 1648
QY 1673 ATTTCTCCGTAAGATCGACACTTATCGAGAACACAGAGCAGTTTGACAGGCTGGATC 1732
DB 1649 ATTTCTCCGTAAGATCGACACTTATCGAGAACACAGAGCAGTTTGACAGGCTGGATC 1708
QY 1733 TTCCATCGGTGTTCACTTGAAAGAGAGTGTACCTTGCCTGTGATACAGTGG 1792
DB 1709 TTCCATCGGTGTTCACTTGAAAGAGAGTGTACCTTGCCTGTGATACAGTGG 1768
QY 1793 TGAATTCGGAAGGCTACGTAGTGAAGAAATCACCATCATGTCCTGGGATTCACGGAGAAA 1852
DB 1769 TGAATTCGGAAGGCTACGTAGTGAAGAAATCACCATCATGTCCTGGGATTCACGGAGAAA 1828
QY 1853 CCGTGGGATACGCGGTTACACAAATAGCGAGGCTTCTTGTAATGCAAAAGTTACTGACA 1912
DB 1829 CCGTGGGATACGCGGTTACACAAATAGCGAGGCTTCTTGTAATGCAAAAGTTACTGACA 1888
QY 1913 CAGTAAAGAGAACGCGGTATCGTTCCCTGTGTGACGTACATCCCGGACCAATATGCG 1972
DB 1889 CAGTAAAGAGAACGCGGTATCGTTCCCTGTGTGACGTACATCCCGGACCAATATGCG 1948
QY 1973 ATCATGATGATGTTATATGAGCCACGGAATATATCACTGACATGCAAAAACCTTTGG 2032
DB 1949 ATCATGATGATGTTATATGAGCCACGGAATATATCACTGACATGCAAAAACCTTTGG 2008
QY 2033 TTGGGCTCAACGAGGATGTCATTAACGGTAGAGTAACAGGAAACCAACCAACATGTC 2092
DB 2009 TTGGGCTCAACGAGGATGTCATTAACGGTAGAGTAACAGGAAACCAACCAACATGTC 2068
QY 2093 AAAATTACTTCTGCGCATCATACAGAGGTTACAGCAATGGGCTTAAGAGCGCAAG 2152
DB 2069 AAAATTACTTCTGCGCATCATACAGAGGTTACAGCAATGGGCTTAAGAGCGCAAG 2128

QY 2153 ATGATCTTGATTAACGAGAAATATCTGGGTAATGAGAACCCAGCTTATGCGTCT 2212
DB 2129 ATGATCTTGATTAACGAGAAATATCTGGGTAATGAGAACCCAGCTTATGCGTCT 2188
QY 2213 TGTGGGCTTGGACATTAAGAAAGTACATTCGTTTATGCGCCACCTGGAACCGACCT 2272
DB 2189 TGTGGGCTTGGACATTAAGAAAGTACATTCGTTTATGCGCCACCTGGAACCGACCT 2248
QY 2273 GCGTAAAGTCCAGGCTCTTTTAAAGCTTTTCCATGTCGTCGTAATGACGACCTT 2332
DB 2249 GCGTAAAGTCCAGGCTCTTTTAAAGCTTTTCCATGTCGTCGTAATGACGACCTT 2308
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DB 2309 TGCCCATGTCGTGAGGACGAAATTTGAATCGGATTCACACCAAGAGAGGAAAAAC 2368
QY 2393 TGCTGACAGGCTCGAGAGGAATTGATGATGAGGACCAAGGCTGCTTTTGAAGATGCTCAG 2452
DB 2369 TGCTGACAGGCTCGAGAGGAATTGATGATGAGGACCAAGGCTGCTTTTGAAGATGCTCAG 2428
QY 2453 AGGAGCCAGAGCGGAGAGAGCTCCGAAAGCATTTCCACATTTAGTGACAGAAAGCA 2512
DB 2429 AGGAGCCAGAGCGGAGAGAGCTCCGAAAGCATTTCCACATTTAGTGACAGAAAGCA 2488
QY 2513 TCGAGGACGCGGACGAAAGTTGTCGGAAGTGAAGGCGCTCCAGGCGGACATGAGACAG 2572
DB 2489 TCGAGGACGCGGACGAAAGTTGTCGGAAGTGAAGGCGCTCCAGGCGGACATGAGACAG 2548
QY 2573 CATTTAGTTGAAACCCCGCGGCTCACGTAAGATTAACCTCAAGCAAAATGACCGTATGA 2632
DB 2549 CATTTAGTTGAAACCCCGCGGCTCACGTAAGATTAACCTCAAGCAAAATGACCGTATGA 2608
QY 2633 TCGGACAGTATATGTTGTCGCAAACTGTGTGTAAGAAATGCAACTGCAACAG 2692
DB 2609 TCGGACAGTATATGTTGTCGCAAACTGTGTGTAAGAAATGCAAACTGCAACAG 2668
QY 2693 CGACCCGCTAGAGATCATGAGTTAATCATTAACAACCTCCGAAATCATGAGAAAGTACG 2752
DB 2669 CGACCCGCTAGAGATCATGAGTTAATCATTAACAACCTCCGAAATCATGAGAAAGTACG 2728
QY 2753 CGGTGCAACATTCAGACGCTTAAAGTACTGATGTCAGACAGAGGTCGCTACATGAGCAG 2812
DB 2729 CGGTGCAACATTCAGACGCTTAAAGTACTGATGTCAGACAGAGGTCGCTACATGAGCAG 2788
QY 2813 AATTCTAGCACTGAGTGAAGCGCCAGTTAGTGTACAAAGAAAGATTTGTGAACC 2872
DB 2789 AATTCTAGCACTGAGTGAAGCGCCAGTTAGTGTACAAAGAAAGATTTGTGAACC 2848
QY 2873 GCAAACTATACCACTTGGCAATGCAATGCGCCCGCCCAAGAAATACAGAAAGAGACATGACA 2932
DB 2849 GCAAACTATACCACTTGGCAATGCAATGCGCCCGCCCAAGAAATACAGAAAGAGACATGACA 2908
QY 2933 AGGTACAAAGGAGAGCTTGCAGAAACAGATGAGTGTGAGCTGTGACAAAGAGGTT 2992
DB 2909 AGGTACAAAGGAGAGCTTGCAGAAACAGATGAGTGTGAGCTGTGACAAAGAGGTT 2968
QY 2993 GCGTTAAGAGAGAGAGCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCTCT 3052
DB 2969 GCGTTAAGAGAGAGAGCTCAGGTCTGCTCTCGGAGAACTGACCAACCTCTCT 3028
QY 3053 ATCATGATGATGCTGAGAGGACCTGAAGACCCGACCTGCGCTACCAAGTGGAAA 3112
DB 3029 ATCATGATGATGCTGAGAGGACCTGAAGACCCGACCTGCGCTACCAAGTGGAAA 3088
QY 3113 CAATAGAGTGAATGAGCACACCGGAGTCCGAGCAAGTCACTATTTCAAGTCAACTGTCA 3172
DB 3089 CAATAGAGTGAATGAGCACACCGGAGTCCGAGCAAGTCACTATTTCAAGTCAACTGTCA 3148
QY 3173 CCGCACGAGATCTTGTACACGCGAAAGAAATTTGTGCGGAATTTGAGCGCGACG 3232
DB 3149 CCGCACGAGATCTTGTACACGCGAAAGAAATTTGTGCGGAATTTGAGCGCGACG 3208
QY 3233 TGCTAAGACTGAGGGGATGACAGATTAAGTCCAGACAGTAAAGTTCGGTTATGCTCAAG 3292

[illegible]

QY 5453 CGGCACTCCAACTTAAGAGACTGTGTAAACAGAGCTGAAGAGATGAATATGAGATCGACG 5512
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QY 5513 ATAGAGTTAGATGAGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 5572
DB 5489 ATAGAGTTAGATGAGATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTA 5548
QY 5573 CAAAGAGAAATTTGATTCCTACTCTCGAAGGACCAAAATTCATCAAGCAGCAAAAGACA 5632
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QY 5633 TGGCGAGATAAAGTCTGTCTCTTAATGACAGAGAAAGTAAAGAACTGTGTGCTT 5692
DB 5609 TGGCGAGATAAAGTCTGTCTCTTAATGACAGAGAAAGTAAAGAACTGTGTGCTT 5668
QY 5693 ACATATTTGGGTGAGACCATGGAAGCAATCCGCGAAAAGTCCCGGTGACACATTAACCGT 5752
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QY 5873 CTAAAGCAAAATTAAGATGTTCAAGAGGTTCAAGTCCAGAAAGTATGCTCTTTAAATC 5932
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QY 5933 CGCACACTCCCGGATTCGTTCCCGCCGTAAGTACATAGAAAGTCCAGAAACAGCTTACG 5992
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DB 6149 CGTCAGAGACTTACTGAGTGTGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 6208
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DB 7289 ACTCAGCGCACTTCAATGTCGAATGCTTCAAAATATGCAATGATATGACGATATGAG 7348
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DB 7409 GACTGAAGAGCCCTTAAAGCCCGCGCACTATTTTTCAGAAAGCGTATATTTTGTGCTCCATG 7468
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DB 7469 AAGAGTGCCTTATGATGATGATTCGTATGATGATGATGATGATGATGATGATGATGATGATG 7528
QY 7553 GCACGAAACACACAG 7612
DB 7529 GCACGAAACACACAG 7588
QY 7613 CGACTGCTTACTTATGCGGGAATTCACCGGGAATTAAGTGCCTTACCGCCGCTTGG 7672

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 VERSION AR282858.1 GI:29719660
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.

REFERENCE 1 (bases 1 to 9951)
 AUTHORS Renner,W.A., Oberberger,G.H., Koller,D. and Bailey,J.E.
 TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
 JOURNAL Patent: US 6524792-A 3 25-FEB-2003;
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ORIGIN

Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
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 Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db	6541	GACTGAAAGGCCCTTAAGGCGCGCCGACATATTGGCAAGAAGCTATTAATTTGGTCCCATTCG	6600
QY	7493	AAGAAGTCCATGATAGATTTCGTCAATGACATGAAAAGACGCGTGAAGTTACACACAG	7552
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QY	7853	CACACTCTGACTGATGCGATGCGCTTTGGAGAAATATATCCACCATCTACCTACGG	7912
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QY	7913	GTACTCGTTTTAAATTGGGGCGATGATGAATTCGGAATGTTCTCTACACTTTTGTCA	7972
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QY	7973	ACACAGTTTTGAATGTGCTTATGCGCGACGAGATCACTAGAAAGCGGCTTAAACGTCGA	8032
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QY	8033	GATGTGACGCGTTCATTGGCGACGACCAATCATATCACTGAGTAGTATCTGACAAAGAA	8092
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QY	8093	TGGCTGAGAGGTGCGCACTGCTCAACATGAGGTTAAAGATCATGACGCACTCATCG	8152
Db	7201	TGGCTGAGAGGTGCGCACTGCTCAACATGAGGTTAAAGATCATGACGCACTCATCG	7260
QY	8153	GTCGAGAACACCTTATCTGCGCGCGGATTTATCTTGGCAAGATTCGGTTACTTCCACAG	8212
Db	7261	GTCGAGAACACCTTATCTGCGCGCGGATTTATCTTGGCAAGATTCGGTTACTTCCACAG	7320
QY	8213	CGTCCCGCGTGGCGGATCCCTGTAAGAAAGCTGTTAAGTGGGTTAAACCGCTCCACACG	8272
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QY	8273	ACGACGACAAAGACGAAGACGAGACGCGCTCTGCTAGATGAACAAAGCGGTGATTGA	8332

Db		7381	ACGAGCAGCAAGACAAGAAACAGGCGCTGTCTAGTAGAACAAGAAGCGTGTTTA	7440	
Oy		8333	GAGTATGGTATAAACAGGCATTTCAGCAGTGGCCGTGACGACCCTGGTATGAGGTAGACATA	83922	
Db		7441	GAGTAGGTATTAACAGGCCACTTTAGCAGTGGCCGTGACGACCCTGGTATGAGGTAGACATA	75000	
Oy		8393	TTACACCTGTCTCTCTGGCATTTGAGAACTTTTGGCCAGAGAAAAGACATTTCCAAGCA	84522	
Db		7501	TTACACCTGTCTCTCTGGCATTTGAGAACTTTTGGCCAGAGAAAAGACATTTCCAAGCA	75600	
Oy		8453	TCAGAGGGGAATAAAGACATCTCTACGGTGGTCCCTAATATAGTCAGCATAGTACATTTTCAT	85122	
Db		7551	TCAGAGGGGAATAAAGACATCTCTACGGTGGTCCCTAATATAGTCAGCATAGTACATTTTCAT	76200	
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DEFINITION	Sequence 2 from Patent WO0130989.				
ACCESSION	AX128602				
VERSION	AX128602.1	GI:14135064			
KEYWORDS					
SOURCE	' synthetic construct				
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 Renner, W.A. and Nieba, L.				
TITLE	Method for creating divergent populations of nucleic acid molecules and proteins				
JOURNAL	Patent: WO 0130989-A 2 03-MAY-2001;				
	Cycos Biotechnology AG (CH) ; Renner, Wolfgang Andreas (CH) ;				
	Nieba, Lars (CH)				
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Db		1	ATTGACGGCGGTATGATCACACTATTGAATCAAAACAGCCGACCAATTTGCACTACATCAACA	60	
Oy		953	TGGAAAGCCGCTACTATAACGTTAGACGTTAGACCCGACAGTCCGTTGTCGCGAATGTC	1012	
Db		61	TGGAAAGCCGCTACTATAACGTTAGACGTTAGACCCGACAGTCCGTTGTCGCGAATGTC	120	
Oy		1013	AAAAAAGCTTCCCGCAATTTTGAAGTAGTAGCAGCAGCAGTCACTCCAATGACCATGCTA	10722	
Db		121	AAAAAAGCTTCCCGCAATTTTGAAGTAGTAGCAGCAGCAGTCACTCCAATGACCATGCTA	180	
Oy		1073	ATGCCAGAGACATTTTCGACTGTGGCCAGTAACTATATGAGCTGAGGTTCCATCAACAG	11322	
Db		181	ATGCCAGAGACATTTTCGACTGTGGCCAGTAACTATATGAGCTGAGGTTCCATCAACAG	240	
Oy		1133	CGACGATCTTGGACATPAGCAGCGGACCGGCTCTGATGATGTTTTCCGAGACCAAGTATC	11922	
Db		241	CGACGATCTTGGACATPAGCAGCGGACCGGCTCTGATGATGTTTTCCGAGACCAAGTATC	300	
Oy		1193	ATTGTGTCTGCCCATTCGCTAGTCCAGAAAGACCCGACCCGACATGATGAATAACGCCAGTA	12522	
Db		301	ATTGTGTCTGCCCATTCGCTAGTCCAGAAAGACCCGACCCGACATGATGAATAACGCCAGTA	360	
Oy		1253	AACTGCGGAAAAAGCGTGCAAGATTACAAACAGAACTTGATGAGAAGATTAAAGATC	13122	

Db	361	AACCTGGCGAATAAGCTGCAAGTTACAAACAAAGAACTTCATGAGAAAGTTAAGATC	420
Oy	1313	TCGCGAACCGTACTTGAATACGCCGGATCTGTAAACACCATCGCTCTGCTTTACACAGATG	1372
Db	421	TCGCGACCGTACTTGAATACGCCGGATCTGTAAACACCATCGCTCTGCTTTACACAGATG	480
Oy	1373	TTACTCTCAACATCCGCTCCGGAATTTCCCTGCATATGCAGACGTGTATATCAACGCTCCG	1432
Db	481	TTACTCTCAACATCCGCTCCGGAATTTCCCTGCATATGCAGACGTGTATATCAACGCTCCG	540
Oy	1433	GAACCTATCTATCATCAGGCTATGAAAGCGGCGGACCCCTGTACTGTGATTTGGCTTCGACA	1492
Db	541	GAACCTATCTATCATCAGGCTATGAAAGCGGCGGACCCCTGTACTGTGATTTGGCTTCGACA	600
Oy	1493	CCACCCAGTTCAATGTTCTCGGCTATGCGAGGTTGTAACCTTCGCTACACACCAACTGGG	1552
Db	601	CCACCCAGTTCAATGTTCTCGGCTATGCGAGGTTGTAACCTTCGCTACACACCAACTGGG	660
Oy	1553	CCGACGAGAAAGTCTTGAAGCGGCTAACATCGACTTTTGACAGACAAAGCTGAGTAAAG	1612
Db	661	CCGACGAGAAAGTCTTGAAGCGGCTAACATCGACTTTTGACAGACAAAGCTGAGTAAAG	720
Oy	1613	GTAGGACAGGAAATTTGTCCGATATATGAGGAAAGAGGTGAAGCCCGGGGTGGGGGTTT	1672
Db	721	GTAGGACAGGAAATTTGTCCGATATATGAGGAAAGAGGTGAAGCCCGGGGTGGGGGTTT	780
Oy	1673	ATTTCTCCGTAGATTCGACACTTTTATCCAGAACACAGAGCCAGCTTCAGAGCTGCATC	1732
Db	781	ATTTCTCCGTAGATTCGACACTTTTATCCAGAACACAGAGCCAGCTTCGAGAGCTGCATC	840
Oy	1733	TTCCATCGGTGTTCATCCTTGATGAGAAAGCATGTCGTACACTTGCCCGCTGTGTATACATGG	1792
Db	841	TTCCATCGGTGTTCACCTTGATGAGAAAGCATGTCGTACACTTGCCCGCTGTGTATACATGG	900
Oy	1793	TGACCTTCGGAAGGCTACGTAGTGAAGAAACACACATCAGTCCGGGATCTACCGGAGAA	1852
Db	901	TGACCTTCGGAAGGCTACGTAGTGAAGAAACACACATCAGTCCGGGATCTACCGGAGAA	960
Oy	1853	CCGTGGGATACGCGGTTTACACACATATGCGAGGCTTTCTTGCTATGCAAAATTACTGACA	1912
Db	961	CCGTGGGATACGCGGTTTACACACATATGCGAGGCTTTCTTGCTATGCAAAATTACTGACA	1020
Oy	1913	CAGTAAAGAGAAACGGGTATGTTCCCTGTGTGCACGTACATCCCGGCCACATATGCG	1972
Db	1021	CAGTAAAGAGAGAACGGGTATGTTCCCTGTGTGCACGTACATCCCGGCCACATATGCG	1080
Oy	1973	ATCAGATGACTGTGTATATATGGCCACCGATATATACCTGACGATGACCAAAACTTCGCG	2032
Db	1081	ATCAGATGACTGTGTATATATGGCCACCGATATATACCTGACGATGACCAAAACTTCGCG	1140
Oy	2033	TTGGGCTCAACACAGCAATTTGCTCATTTAACGGTAAAGACTTACAGGAAACCAACACATGC	2092
Db	1141	TTGGGCTCAACACAGCAATTTGCTCATTTAACGGTAAAGACTTACAGGAAACCAACACATGC	1200
Oy	2093	AAAAATTACCTTCTGCCGATCATATGACACAGGGTTTCAAGCAATTTGGCTTAAGAGCGCAAG	2152
Db	1201	AAAAATTACCTTCTGCCGATCATATGACACAGGGTTTCAAGCAATTTGGCTTAAGAGCGCAAG	1260
Oy	2153	ATGATCTTGATATACGAGAAATGCTGTGGTACTAAGAAACCGAACCTTATCGTATGGCTGCT	2212
Db	1261	ATGATCTTGATATACGAGAAATGCTGTGGTACTAAGAAACCGAACCTTATCGTATGGCTGCT	1320
Oy	2213	TGTGGGCGCTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGCAAGCT	2272
Db	1321	TGTGGGCGCTTTCGCACTAAGAAAGTACATTCGTTTATCGCCCACTGGAACGCAAGCT	1380
Oy	2273	GCCTAATAAGTCCAGCCTCTTTTATGCGCTTTTCCCATGTGCTCCGTATGACGACTCTT	2332
Db	1381	GCCTAATAAGTCCAGCCTCTTTTATGCGCTTTTCCCATGTGCTCCGTATGACGACTCTT	1440
Oy	2333	TGCCCATGTGCTGTAGGAGAAATTTGAACCTGCACTTGACACCAAGAAAGAGAAAC	2392

Db	1441	TCGCCATGTGCGCTGAGCGAGAAATTGAAACTGCGACTTTGCCAACCAGAAAGAGGAAAAAC	1500
Qy	2393	TGCTGCGAGGTCCTCGAGGAATTAGTCATGAGAGCCAGGCTGCTTTGAGATGCTCAGG	2452
Db	1501	TGCTGCGAGGTCCTCGAGGAATTAGTCATGAGAGCCAGGCTGCTTTGAGATGCTCAGG	1560
Qy	2453	AGGAAGCCGAGCGGAGAGAGCTCCGAGAGAGCACTTCCACTTGTGTGCGACAGAAAGCA	2512
Db	1561	AGGAAGCCGAGCGGAGAGAGCTCCGAGAGAGCACTTCCACTTGTGTGCGACAGAAAGCA	1620
Qy	2513	TCGAGGCGAGCCGAGAAAGTTGTCGCAAGTGAAGGGGCTCCAGGCGAGCATCGGAGAG	2572
Db	1621	TCGAGGCGAGCCGAGAAAGTTGTCGCGAAGTGAAGGGGCTCCAGGCGAGCATCGGAGAG	1680
Qy	2573	CATTAGTTGAACCCCGCGCGGTCACTGAAGATATATCTTCAAGCAAAATGACCGTATGA	2632
Db	1681	CATTAGTTGAACCCCGCGCGGTCACTGAAGATATATCTTCAAGCAAAATGACCGTATGA	1740
Qy	2633	TCGGACAGTATATGTTGTCCTGCGCAACTCTGTGCTGTAAGAAATGCCAACTTCGCAACG	2692
Db	1741	TCGGACAGTATATGTTGTCCTGCGCAACTCTGTGCTGTAAGAAATGCCAACTTCGCAACG	1800
Qy	2693	CGCACCCGCGTAGAGATCAGGTTAAGATCATATACACTCCGGAAGATCAGGAAGTATCG	2752
Db	1801	CGCACCCGCGTAGAGATCAGGTTAAGATCATATACACTCCGGAAGATCAGGAAGTATCG	1860
Qy	2753	CGGTGGAACCATACGACGCGTAAAGTACTGATGCGACGAGAGGTGCGGTACATGGCCAG	2812
Db	1861	CGGTGGAACCATACGACGCGTAAAGTACTGATGCGACGAGAGGTGCGGTACATGGCCAG	1920
Qy	2813	AATTCCCTTAGCACTGAGTGAAGAGCCGCACAGTTAGTGTACACAGAAAGAGATTTGTGAAC	2872
Db	1921	AATTCCCTTAGCACTGAGTGAAGAGCCGCACAGTTAGTGTACACAGAAAGAGATTTGTGAAC	1980
Qy	2873	GCAAACTATACCACTTGTCCATGCTGAGTGGCCCCGCAAGAAATACAGAGAGGACAGTACA	2932
Db	1981	GCAAACTATACCACTTGTCCATGCTGAGTGGCCCCGCAAGAAATACAGAGAGGACAGTACA	2040
Qy	2933	AGGTTACAAAGGCGAGAGCTTGCAGAAACAGAGTACGTGTTTACAGCTGAGCAAGAGCGTT	2992
Db	2041	AGGTTACAAAGGCGAGAGCTTGCAGAAACAGAGTACGTGTTTACAGCTGAGCAAGAGCGTT	2100
Qy	2993	GCCTTTAAGAGGAAGAAAGCTTCAGGTCGTGTCCTCGGAGAACTGACCAACCTCCCT	3052
Db	2101	GCCTTTAAGAGGAAGAAAGCTTCAGGTCGTGTCCTCGGAGAACTGACCAACCTCCCT	2160
Qy	3053	ATCATGAGCTATGCTCTGGAGGGAGCTGAAAGACCCGACCTGGGCTCCCGTACAAAGTTCGAA	3112
Db	2161	ATCATGAGCTATGCTCTGGAGGGAGCTGAAAGACCCGACCTGGGCTCCCGTACAAAGTTCGAA	2220
Qy	3113	CAATAGAGTGAATGCGACACCGGGGTCGGGCAAGTCAGTATTTATCAAGTCAACTGTCA	3172
Db	2221	CAATAGAGTGAATGCGACACCGGGGTCGGGCAAGTCAGTATTTATCAAGTCAACTGTCA	2280
Qy	3173	CGGACCGAGATCTTGTTTACAGCGGAAAGAAATTTGTCGGAATTTGAGCCGACG	3232
Db	2281	CGGACCGAGATCTTGTTTACAGCGGAAAGAAATTTGTCGGAATTTGAGCCGACG	2340
Qy	3233	TGCTTAAGCTGAGGGGATATGCAATTCAGTTCGGAAGACAGTATTCGGTTATGCTCAACG	3292
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Qy	3293	GATGCCACAAAGCCGTAAGATGCTGTATCCTTGAAGAGCGTTGCGGTGCGACGACGAGAG	3352
Db	2401	GATGCCACAAAGCCGTAAGATGCTGTATCCTTGAAGAGCGTTGCGGTGCGACGACGAGAG	2460
Qy	3353	CACCTACTTGCTTATTTGCTATGCTCAGGCCCCGCAAGAGAGTATGCTATGCGAGAAC	3412
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Qy	3413	CCATGCAATGCGGATCTTCAACATGATGACCACTTAAAGTACATTTCAATACCTTGAA	3472
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QY	3473	TAAGCATATGACCAACAACATTCGCAAGATATCTCCGGCGTTGACACAGCACAATT	3552
Db	2561	AAGCATATGACCAAGACATTTCAACAAGTATCTCCGGCGTTGACACAGCACAATT	2640
QY	3533	CAGCTATTGTATCGACACTGATACATTCAGTGGAAAGATGAAACCCACGACCCTGCAGA	3592
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QY	3893	TACCTAAAGGAACTTTTCAGGCTATCTATAGAGACTGGAAAGCTGAAACAAGGAAATTA	3952
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QY	3953	TTGCTGAATTAACAGGCCCACTCCCGTCCCAATCCGTTCAAGCTGAAACCAACGTTT	4012
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 ORGANISM Unknown.

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 AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
 TITLE Expression cloning processes for the discovery, characterization
 and isolation of genes encoding polypeptides with a predetermined
 property

Patent: US 6524792-A 4-25-FEB-2003;

JOURNAL
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 AR282860
 LOCUS AR282860 11927 bp DNA 11near PAT 10-Apr-2003
 DEFINITION Sequence 5 from patent US 6524792.
 ACCESSION AR282860
 VERSION AR282860.1 GI:29719662
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 11927)
 AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
 TITLE Expression cloning processes for the discovery, characterization and isolation of genes encoding polypeptides with a predetermined property
 JOURNAL Patent: US 6524792-A 5 25-FEB-2003;
 FEATURES Location/Qualifiers
 source 1..11927 /organism="unknown" /mol_type="genomic DNA"
 ORIGIN
 Query Match 89.4%; Score 7637.4; DB 6; Length 11927;
 Best Local Similarity 99.9%; Pred. No. 0;
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Oy	6053	CTGATTAACACCTCGGTGATGTCACAGACATCTCACTGGATATGGAATCATAGTAGCGAAG	6112
Db	5161	CTGATTAACACCTCGGTGATGTCACAGACATCTCACTGGATATGGAATCATAGTAGCGAAG	5220
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DEFINITION ARI37241
ACCESSION ARI37241
VERSION ARI37241.1 GI:14478750
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 13905)
AUTHORS Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.
TITLE Expression cloning processes for the discovery characterization,
and isolation of genes encoding polypeptides with a predetermined
property
JOURNAL Patent: US 6197502-A 1 06-MAR-2001;
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ORIGIN

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Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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VERSION AR282856.1 GI:29719658
KEYWORDS
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REFERENCE 1 (bases 1 to 13905)
Renner, W.A., Orberger, G.H., Koller, D. and Bailey, J.E.

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ORIGIN

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SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 8000)
AUTHORS Dubensky,T.W., Jr., Polo,J.M., Schlesinger,S. and Frolov,I.
TITLE Alphavirus structural protein expression cassettes
JOURNAL Patent: US 6426196-A 102 30-JUL-2002;
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source location/Qualifiers
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 ORGANISM Crassostrea virginica
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REFERENCE 1 (bases 1 to 860)
 Jenny, M.J., Marr, G.W., Gross, P.S., Almeida, J.S., Chen, Y.,
 McKillen, D.J., Wu, S., and Chapman, R.M.

Crassostrea virginica EST library at marinesgenomics.org
 Unpublished (2004)
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 Tel: 843 792 8503
 Fax: 843 792 4850

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 Best Local Similarity 97.4%; Pred. No. 1.6e-174;
 Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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 DB 647 GCTACACTTCCAGCGCGCATTTAGCGCGCGGTGTGTGTGTTACGCGCAGCGTGACC 588
 QY 123 ACGTTCCCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 182
 DB 587 ACGTTCCCGCGCTTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATTT 528
 QY 183 AGTGCCTTTAGGGAGCGCGCATTTAGCGCGCGGTGTGTGTGTTACGCGCAGCGTGACC 242
 DB 527 AGTGCCTTTAGGGAGCGCGCATTTAGCGCGCGGTGTGTGTGTTACGCGCAGCGTGACC 468
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 QY 303 GGAAGCTTTGTTCCAACTGGAACAACACTCAACCTTATCTCGGTCTAATTTCTTTGATTTA 362
 DB 407 GGAAGCTTTGTTCCAACTGGAACAACACTCAACCTTATCTCGGTCTAATTTCTTTGATTTA 348
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 QY 483 ACTGTTGGGAAGGCGCATTCGTCGGGGCTCTTTCGCTATTACGCCAGCTGGCGAAAGGGG 542
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 QY 543 GATGTCGTCAAGGCGATTTAGTTGGGTAAAGCGCAGGGTTTCCCATGACGACGCTTTGA 602
 DB 167 GATGTCGTCAAGGCGATTTAGTTGGGTAAAGCGCAGGGTTTCCCATGACGACGCTTTGA 108
 QY 603 AAACGACGCGCAGTGAGCGCGCAATTAAACCTTCATTAAGGAA 646
 DB 107 AAACGACGCGCAGTGAGCGCGCAATTAAACCTTCATTAAGGCGCA 64

RESULT 3
 CN385663 862 bp mRNA linear EST 31-AUG-2004
 LOCUS LE2TR04D12 Tomato CL5915 roots under different developmental stages
 DEFINITION Lycopersicon esculentum cDNA clone LE2TR04D12, mRNA sequence.

ACCESSION CN385663
 VERSION CN385663.1 GI:51700977
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicot;
 asterids; Lamiales; Solanales; Solanales; Solanaceae; Solanum; Lycopersicon.

REFERENCE 1 (bases 1 to 862)
AUTHORS Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
TITLE DNA microarray profiling of gene expression during tomato root development
JOURNAL Unpublished (2004)
COMMENT Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Biagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2651-5600
Email: kyoo@ate.sinica.edu.tw
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ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 862;
Best Local Similarity 97.4%; Pred. No. 1.6e-174;
Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 699 GACCGCGCCGTGTACGGCGCATTAAGCGCGCGGTGTGTGTACCGCGAGGTACC 640
QY 63 GCTACACTTGTGCAGCGCCTTAGCGCGCCTTCTTCTTCTTCTTCTTCTTCTG 122
Db 639 GCTACACTTGTGCAGCGCCTTAGCGCGCCTTCTTCTTCTTCTTCTTCTTCTG 580
QY 123 ACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCG 182
Db 579 ACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCG 520
QY 183 AGTGTCTTACGGGCACTTCGACCCCAAAAACCTTATAGGTGATGTTCACTAGTGG 242
Db 519 AGTGTCTTACGGGCACTTCGACCCCAAAAACCTTATAGGTGATGTTCACTAGTGG 460
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Db 459 CCATCGCGCCTGATAGAGGTTTTCGCGCTTGTGAGTGCACGTTCTTATATAGT 400
QY 303 GGAAGCTTGTTCGAACTGGAACAACACTCAACCTTATCTGTGCTATCTTTGATTTA 362
Db 399 GGAAGCTTGTTCGAACTGGAACAACACTCAACCTTATCTGTGCTATCTTTGATTTA 340
QY 363 TAAAGGATTTTTCGCGCTTATGTTGTTAAAAAATAGTGCATTTAACAATAATTT 422
Db 339 TAAAGGATTTTTCGCGCTTATGTTGTTAAAAAATAGTGCATTTAACAATAATTT 280
QY 423 AACGCAATTTTAAACAATAATTAAGCTTACATTTCCATTCGCAATTCAGGCTGCGCA 482
Db 279 AACGCAATTTTAAACAATAATTAAGCTTACATTTCCATTCGCAATTCAGGCTGCGCA 220
QY 483 ACTGTGGGAAGGCGATCGGTGCGGGCTCTTCTGCTATTAAGCAGTGGCGAAAGGG 542
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QY 543 GATGTGTGCAAGCGCATTAAGTTGAGTAAAGCCAGGAGTTTCCCACTACAGAGTTGTA 602
Db 159 GATGTGTGCAAGCGCATTAAGTTGAGTAAAGCCAGGAGTTTCCCACTACAGAGTTGTA 100
QY 603 AAACGACGCGCAGTACGCGCATTAACCTTCACTAAAGGAA 646
Db 99 AAACGACGCGCAGTACGCGCATTAAGTAAATACGATCACTATAGGCGCAA 56

RESULT 4
CN385637/c
LOCUS LE2TR04C09 Tomato CL5915 roots under different developmental stages
DEFINITION Lycopersicon esculentum cDNA clone LE2TR04C09, mRNA sequence.
ACCESSION CN385637
VERSION CN385637.1 GI:51700951
KEYWORDS EST.
SOURCE Lycopersicon esculentum (tomato)
ORGANISM Lycopersicon esculentum
Bikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 874)
Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
DNA microarray profiling of gene expression during tomato root development
Unpublished (2004)
Contact: Kin-Ying, To
Crop Plant Improvement Group
Institute of Biagricultural Sciences, Academia Sinica
128 Academia Rd. Section 2, Taipei, Taiwan 11529
Tel: 886-2-2653-3161
Fax: 886-2-2651-5600
Email: kyoo@ate.sinica.edu.tw
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/dev_stage="1-,2-,3-, and 4- month-old"
/lab_host="E.coli BM25.8"
/clone_id="Tomato CL5915 roots under different developmental stages"
/note="Vector: pTriplex2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA Library construction kit, Clontech)."

FEATURES

Source

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QY 3 GAGCGCGCCGTGTACGGCGCATTAAGCGCGCGGTGTGTGTACCGCGAGGTACC 62
Db 699 GACCGCGCCGTGTACGGCGCATTAAGCGCGCGGTGTGTGTACCGCGAGGTACC 640
QY 63 GCTACACTTGTGCAGCGCCTTAGCGCGCCTTCTTCTTCTTCTTCTTCTTCTG 122
Db 639 GCTACACTTGTGCAGCGCCTTAGCGCGCCTTCTTCTTCTTCTTCTTCTTCTG 580
QY 123 ACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCG 182
Db 579 ACGTTGCGCGCTTCCCGCTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCG 520
QY 183 AGTGTCTTACGGGCACTTCGACCCCAAAAACCTTATAGGTGATGTTCACTAGTGG 242
Db 519 AGTGTCTTACGGGCACTTCGACCCCAAAAACCTTATAGGTGATGTTCACTAGTGG 460
QY 243 CCATCGCGCCTGATAGAGGTTTTCGCGCTTGTGAGTGCACGTTCTTATATAGT 302
Db 459 CCATCGCGCCTGATAGAGGTTTTCGCGCTTGTGAGTGCACGTTCTTATATAGT 400
QY 303 GGAAGCTTGTTCGAACTGGAACAACACTCAACCTTATCTGTGCTATCTTTGATTTA 362
Db 399 GGAAGCTTGTTCGAACTGGAACAACACTCAACCTTATCTGTGCTATCTTTGATTTA 340
QY 363 TAAAGGATTTTTCGCGCTTATGTTGTTAAAAAATAGTGCATTTAACAATAATTT 422
Db 339 TAAAGGATTTTTCGCGCTTATGTTGTTAAAAAATAGTGCATTTAACAATAATTT 280
QY 423 AACGCAATTTTAAACAATAATTAAGCTTACATTTCCATTCGCAATTCAGGCTGCGCA 482
Db 279 AACGCAATTTTAAACAATAATTAAGCTTACATTTCCATTCGCAATTCAGGCTGCGCA 220
QY 483 ACTGTGGGAAGGCGATCGGTGCGGGCTCTTCTGCTATTAAGCAGTGGCGAAAGGG 542
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Db 579 ACGTTCGCGGCTTCCCGCTCAAGCTCTAAATCGGGGCTCCCTTAGGGTTCCGATTT 520

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Db 519 AGTGCCTTACGGCACTCGACCCCAAAAACCTGATTAGGTGATGTTCACTAGTGGG 460

Qy 243 CCATCGCCCTGATGAGGGTTTTTCGCCCTTTGACGTTGAGTCCAGTCTTTAATAGT 302

Db 459 CCATCGCCCTGATGAGGGTTTTTCGCCCTTTGACGTTGAGTCCAGTCTTTAATAGT 400

Qy 303 GGACTCTGTTCCAACTGGAACAACCTCAACCTTATCTCGGCTATCTTTGATTGA 362

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Qy 363 TAAAGGATTTTCCGATTTCCGCTATTGTTAAATAAGAGTGAATTAACAAAATTT 422

Db 339 TAAAGGATTTTCCGATTTCCGCTATTGTTAAATAAGAGTGAATTAACAAAATTT 280

Qy 423 AACGCGAATTTTAAACAAATTTTAAGCTTCAATTTTCATGCGCATTCAGGCTGCGCA 482

Db 279 AACGCGAATTTTAAACAAATTTTAAGCTTCAATTTTCATGCGCATTCAGGCTGCGCA 220

Qy 483 ACTGTTGGGAAGGCGATCGGTCGGGCTCTTGCTATTATTAAGCAGCTGGCGAAAGGG 542

Db 219 ACTGTTGGGAAGGCGATCGGTCGGGCTCTTGCTATTATTAAGCAGCTGGCGAAAGGG 160

Qy 543 GATGTCGTCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTCAAGAGTTGTA 602

Db 159 GATGTCGTCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTCAAGAGTTGTA 100

Qy 603 AAACGACGCGCAGTGAATGTGTAATACGACTCATTAAGGGA 646

Db 99 AAACGACGCGCAGTGAATGTGTAATACGACTCATTAAGGCGAA 56

RESULT 5
CN385877/c 884 bp mRNA linear EST 31-AUG-2004

LOCUS LE2TR04M16 Tomato CL5915 roots under different developmental stages

DEFINITION Lycopersicon esculentum cDNA clone LE2TR04M16, mRNA sequence.

ACCESSION CN385877

VERSION CN385877.1 GI:51701191

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y. DNA microarray profiling of gene expression during tomato root development

AUTHORS Unpublished (2004)

TITLE Contact: Kin-Ying, To

JOURNAL Crop Plant Improvement Group

COMMENT Institute of Biotechnology Sciences, Academia Sinica

128 Academia Rd. Section 2, Taipei, Taiwan 11529

Tel: 886-2-2653-3161

Fax: 886-2-2651-5600

Email: kyto@gate.sinica.edu.tw

Insert Length: 884 Std Error: 0.00

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Seq primer: smact2

FEATURES

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1. .884

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/note="Vector: pTriplex2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-2-3-4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA library construction kit, Clontech)"

ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 884;

Best Local Similarity 97.4%; Pred. No. 1.6e-174;

Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 3 GAGCGCCCTGTAGGCGGCGCATTAAGCGGGGGGTGTGTGTTTACGCGACGCGAC 62

Db 699 GAGCGCCCTGTAGGCGGCGCATTAAGCGGGGGGTGTGTGTTTACGCGACGCGAC 640

Qy 63 GCTACACTTCCAGCGCGCCCTAGCGCCCGCTCTTTCCTTCCCTTCTTCCGCC 122

Db 639 GCTACACTTCCAGCGCGCCCTAGCGCCCGCTCTTTCCTTCCCTTCTTCCGCC 580

Qy 123 ACGTTCGCGGCTTCCCGCTTCCGCTTCAATTCGGGGGCTCCCTTAGGCTTCCGATT 182

Db 579 ACGTTCGCGGCTTCCCGCTTCCGCTTCAATTCGGGGGCTCCCTTAGGCTTCCGATT 520

Qy 183 AGTGTCTTACGCGCACCTCGACCCCAAAAACCTGATTAGGGGTAGTGTTCAGTATGG 242

Db 519 AGTGTCTTACGCGCACCTCGACCCCAAAAACCTGATTAGGGGTAGTGTTCAGTATGG 460

Qy 243 CCATGCGCCTGATGACGAGTTTTCGCTTTCGAGCTTGAAGTCAAGCTTTTAATAGT 302

Db 459 CCATGCGCCTGATGACGAGTTTTCGCTTTCGAGCTTGAAGTCAAGCTTTTAATAGT 400

Qy 303 GGACTCTGTTCCAACTGGAACAACCTCAACCTTATCTCGGCTATCTTTGATTGA 362

Db 399 GGACTCTGTTCCAACTGGAACAACCTCAACCTTATCTCGGCTATCTTTGATTGA 340

Qy 363 TAAAGGATTTTCCGATTTCCGCTATTGTTAAATAAGAGTGAATTAACAAAATTT 422

Db 339 TAAAGGATTTTCCGATTTCCGCTATTGTTAAATAAGAGTGAATTAACAAAATTT 280

Qy 423 AACGCGAATTTTAAACAAATTTTAAGCTTCAATTTTCATGCGCATTCAGGCTGCGCA 482

Db 279 AACGCGAATTTTAAACAAATTTTAAGCTTCAATTTTCATGCGCATTCAGGCTGCGCA 220

Qy 483 ACTGTTGGGAAGGCGATCGGTCGGGCTCTTGCTATTATTAAGCAGCTGGCGAAAGGG 542

Db 219 ACTGTTGGGAAGGCGATCGGTCGGGCTCTTGCTATTATTAAGCAGCTGGCGAAAGGG 160

Qy 543 GATGTCGTCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTCAAGAGTTGTA 602

Db 159 GATGTCGTCAAGGCGATTAAAGTTGGGTAAAGCCAGGGTTTTCCAGTCAAGAGTTGTA 100

Qy 603 AAACGACGCGCAGTGAATGTGTAATACGACTCATTAAGGGA 646

Db 99 AAACGACGCGCAGTGAATGTGTAATACGACTCATTAAGGCGAA 56

RESULT 6
CN385574/c 899 bp mRNA linear EST 31-AUG-2004

LOCUS LE2TR03P18 Tomato CL5915 roots under different developmental stages

DEFINITION Lycopersicon esculentum cDNA clone LE2TR03P18, mRNA sequence.

ACCESSION CN385574

VERSION CN385574.1 GI:51700888

KEYWORDS EST.

SOURCE Lycopersicon esculentum (tomato)

ORGANISM Lycopersicon esculentum

REFERENCE Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y. DNA microarray profiling of gene expression during tomato root development

AUTHORS Unpublished (2004)

TITLE Contact: Kin-Ying, To

JOURNAL Crop Plant Improvement Group

COMMENT Institute of Biotechnology Sciences, Academia Sinica

128 Academia Rd. Section 2, Taipei, Taiwan 11529

Tel: 886-2-2653-3161

Fax: 886-2-2651-5600

Email: kyto@gate.sinica.edu.tw

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FEATURES

source

1. .884

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/dev_stage="1-2-3-4-month-old"

/lab_host="E.coli BM25.8"

AUTHORS Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
 TITLE DNA microarray profiling of gene expression during tomato root development
 JOURNAL Unpublished (2004)
 COMMENT Contact: Kin-Ying, To
 Crop Plant Improvement Group
 Institute of BioAgricultural Sciences, Academia Sinica
 128 Academia Rd. Section 2, Taipei, Taiwan 11529
 Tel: 886-2-2653-3161
 Fax: 886-2-2561-5600
 Email: kyto@gate.sinica.edu.tw
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 Seq primer: smart2.
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 /clone_id="Tomato CL5915 roots under different developmental stages"
 /note="Vector: pTRIPLEX2; Tomato CL5915 seeds are obtained from AVRDC. Roots were harvested from plants grown under different developmental stages: 1-,2-,3-,4-month-old. Equal aliquots of mRNA of different developmental stages were mixed and used for cDNA library construction. (Smart PCR cDNA library construction kit, Clontech)"

ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 899;
 Best Local Similarity 97.4%; Pred. No. 1.6e-174;
 Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Qy 3 GAGCGCGCCGTAGCGGCGCATTTAAGCGCGCGGTGTGGTTAGCGCGAGCGTACC 62
Db 699 GAGCGCGCCGTAGCGGCGCATTTAAGCGCGCGGTGTGGTTAGCGCGAGCGTACC 640
Qy 63 GCTACACTTCCAGCGCGCCTTAGCGCCGCTCTTTCGCTTTCCTTCTCGCC 122
Db 639 GCTACACTTCCAGCGCGCCTTAGCGCCGCTCTTTCGCTTTCCTTCTCGCC 580
Qy 123 ACGTTGCCGCGCTTTCCTCGCTCAAGCTCTAATCGGCGGCTCCCTTTAGGGTTCCGATT 182
Db 579 ACGTTGCCGCGCTTTCCTCGCTCAAGCTCTAATCGGCGGCTCCCTTTAGGGTTCCGATT 520
Qy 183 AGTGCCTTAGGCGACCTCGAACCCCAAAACTGATTAGGTTGATGCTTCACTGATGGG 242
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Qy 423 AACCGAATTTTAAACAAATTTAAGCTTAACTTCAATTCGCACTTCAGGCTGGCA 482
Db 279 AACCGAATTTTAAACAAATTTAAGCTTAACTTCAATTCGCACTTCAGGCTGGCA 220
Qy 483 ACTGTTGGGAAAGGCGATCGGTGCGGCTCTTTCGCTATTAGCGCAAGTGGCGAAAGGG 542
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Qy 543 GATGCTGCAGGCGCATTTAAGTTGGTTAAGCGCAGGCTTTCCAGTCAAGCTTTGA 602
 Db 159 GATGCTGCAGGCGCATTTAAGTTGGTTAAGCGCAGGCTTTCCAGTCAAGCTTTGA 100

Qy 603 AAACGACGGCCAGTACCGCGCATTTAACCTTCACTTAAGGAA 646
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RESULT 7
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 LOCUS LE2TR01A01 Tomato CL5915 roots under different developmental stages
 DEFINITION Lycopersicon esculentum cDNA clone LE2TR01A01, mRNA sequence.
 ACCESSION CN384456
 VERSION CN384456.1 GI:51699770
 KEYWORDS EST.
 SOURCE Lycopersicon esculentum (tomato)
 ORGANISM Lycopersicon esculentum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 1 (bases 1 to 921)
 Wang, C.K., Chen, P.Y., Wang, H.M., Soong, S.C., Chen, S.C. and To, K.Y.
 TITLE DNA microarray profiling of gene expression during tomato root development
 JOURNAL Unpublished (2004)
 COMMENT Contact: Kin-Ying, To
 Crop Plant Improvement Group
 Institute of BioAgricultural Sciences, Academia Sinica
 128 Academia Rd. Section 2, Taipei, Taiwan 11529
 Tel: 886-2-2653-3161
 Fax: 886-2-2561-5600
 Email: kyto@gate.sinica.edu.tw
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 Seq primer: smart2.
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ORIGIN

Query Match 7.2%; Score 616.8; DB 7; Length 921;
 Best Local Similarity 97.4%; Pred. No. 1.6e-174;
 Matches 627; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

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Db 699 GAGCGCGCCGTAGCGGCGCATTTAAGCGCGCGGTGTGGTTAGCGCGAGCGTACC 640
Qy 63 GCTACACTTCCAGCGCGCCTTAGCGCCGCTCTTTCGCTTTCCTTCTCGCC 122
Db 639 GCTACACTTCCAGCGCGCCTTAGCGCCGCTCTTTCGCTTTCCTTCTCGCC 580
Qy 123 ACGTTGCCGCGCTTTCCTCGCTCAAGCTCTAATCGGCGGCTCCCTTTAGGGTTCCGATT 182
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OY	603	AAACGACGGCCAGTACGGCCGCAATTAACCTCAGTAAAGGAA	646
Db	99	AAACGACGGCCAGTAAATTGTAATACGATCTAATTAAGGGCGAA	56

RESULT 8	BE421195/c	805 bp	mRNA	linear	EST 24-JUL-2000
LOCUS					
DEFINITION	HM0006.G08 TREC HMM Barley leaf library Hordeum vulgare subsp. vulgare cDNA clone HM0006.G08, mRNA sequence.				
ACCESSION	BE421195				

ACCESSION	BE421195
VERSION	BE421195.1
KEYWORDS	GI:9419038
SOURCE	EST.
ORGANISM	<i>Hordeum vulgare</i> subsp. <i>vulgare</i> <i>Hordeum vulgare</i> subsp. <i>vulgare</i>

REFERENCE
AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
1 (baes 1 to 805)
Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T.,

TITLE	JOURNAL	COMMENT
Glautier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafsson, P., Hermann, R.G., Holton, T., Jacquemund, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shieriflou, M., Sorrells, M., Wadburton, M. and Weizel, G.	International Triticeae ESI Cooperative (ITEC)	Production of Expressed Sequence Tags for Species of the Triticeae
Unpublished (2000)		
Contact: Hermann RG		

Botanisches Institut der LMU
Menzinger Str. 67, D-80638 München GERMANY
Fax: 49 30 171683
Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
<http://wheat.pw.usda.gov/genome>.

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FEATURES
  source
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        /organism="Hordium vulgare subsp. vulgare"
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/clone lib= "rpec HMM Barley Leaf Library"
/note= "Vector: pBluescriptSK(-); 850 bp average insert
size."

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Qy	1	CTGACGCGCCCTGTAGCGGCGATTAAAGCGGCGGGGTGTGGATTACGGCGACAGCTGA	60
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Qy	61	CCGCTACACTTTGCCAGGGCCCTACGGCCGCTCTTTCGCTTTTCCTTCCTTCCTTCG	120
Db	717	CCGCTACACTTTGCCAGGGCCCTACGGCCGCTCTTTCGCTTTTCCTTCCTTCCTTCG	658
Qy	121	CCAGCTTCGCGCGCTTTCCCGTCAGACTCTAAATCGGGGCGCTCCCTTTAGGTTCCGAT	180
Db	657	CCAGCTTCGCGCGGCTTTCCCGTCAGACTCTAAATCGGGGCGCTCCCTTTAGGTTCCGAT	598
Qy	181	TTAGTGCCTTAACGGACCTTGACCCCAAAAACTTGATTAGGGTGAATGTTCAAGTAGTG	240
Db	597	TTAGTGCCTTAACGGACCTTGACCCCAAAAACTTGATTAGGGTGAATGTTCAAGTAGTG	538
Qy	241	GGCGATCGCCCTGTAGACGATTTTTCGCGCTTTGAGCTTGAGAGTCAAGTTCTTTAATA	300
Db	537	GGCGATCGCCCTGTAGACGATTTTTCGCGCTTTGAGCTTGAGAGTCAAGTTCTTTAATA	478
Qy	301	GTGACCTCTTGTTCGAAACTGGAACAACACTCAACCTCATCTCGGTATTCCTTTGATT	360
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Qy	361	TATAAGGATTTTTCGCAATTCGGCTCATTTGGTT-AAAAATAGAGTATTAACAAAA	419
Db	417	TATAAGGATTTTTCGCAATTCGGCTCATTTGGTTAAAAAAAATAGAGTATTAACAAAA	358
Qy	420	TTTAAACGCAATTTTAACAAAATTTAAGCTTACAAATTCATTCAGTTCGCATTCAGGCTGC	479
Db	357	TTTAAACGCAATTTTAACAAAATTTAAGCTTACAAATTCATTCAGTTCGCATTCAGGCTGC	298
Qy	480	GCAACTGTTGGGAAAGGGCGATCGGTGGGGGCTTCCTGCTATTACGCGACAGTGGCGAAAG	539
Db	297	GCAACTGTTGGGAAAGGGCGATCGGTGGGGGCTTCCTGCTATTACGCGACAGTGGCGAAAG	238
Qy	540	GGGATGTGCTGCAGAGCGATTAAATTGGGTTAACGCGACAGGATTTTCCCAGTCAAGAGTT	599
Db	237	GGGATGTGCTGCAGAGCGATTAAATTGGGTTAACGCGACAGGATTTTCCCAGTCAAGAGTT	178
Qy	600	GTAAAAAGAGCGCGCACTGACGGCGC	624
Db	177	GTAAAAAGAGCGCGCACTGACGGCGC	153

RESULT 9	
LOCUS	BUT724260/c
DEFINITION	685 bp mRNA linear EST 23-OCT-2003 BUT724260 SIM Schistosoma japonicum cDNA similar to gb AB53629.1 (U844006) beta-galactosidase [Expression vector pBSIT-LUCINT], mRNA sequence.
ACCESSION	BUT724260
VERSION	BUT724260.1 GI:28331629
KEYWORDS	EST.
SOURCE	Schistosoma japonicum
ORGANISM	Schistosoma japonicum
REFERENCE	Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeida; Schistosomatoidae; Schistosomatiidae; Schistosoma. 1 (bases 1 to 685)
AUTHORS	Hu,W., Fan,Q., Shen,D.K., Liu,F., Zhu,Z.D., Song,H.D., Xu,X.R., Wang,Z.J., Kong,Y.P., Zeng,L.C., Wu,J., Zhang,X., Wang,J.J., Xu,X.N., Wang,S.Y., Fu,G., Zhang,X.L., Wang,Z.Q., Brindley,P.J., McManus,B.P., Xue,C.L., Feng,Z., Chen,Z. and Han,Z.G.

TITLE Evolutionary and biomedical implications of a *Schistosoma japonicum* complementary DNA resource
JOURNAL Nat. Genet. 35 (2), 139-147 (2003)
MEDLINE 22879925
PUBMED 12973349
COMMENT Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn.
Location/Qualifiers
FEATURES
source
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/mol_type="mRNA"
/db_xref="taxon:6182"
/sex="male"
/issue_type="whole body"
/dev_stage="adult"
/lab_host="rabbits"
/clone_lib="SJM"

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Query Match 7.1%; Score 607.8; DB 5; Length 685;
Best Local Similarity 97.2%; Pred. No. 7.9e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

1 CTGACGGCCCTGTAGCGGCGCATTAAGCGGGGGTGTGTGTATACCGCAGCGTGA 60
675 CTGACGGCCCTGTAGCGGCGCATTAAGCGGGGGTGTGTGTATACCGCAGCGTGA 616
61 CCGGTACACTTGGCAGGCGCCCTAGCGCGGCTCTTTCGCTTTCCTTCCTTCTCG 120
615 CCGGTACACTTGGCAGGCGCCCTAGCGCGGCTCTTTCGCTTTCCTTCCTTCTCG 556
121 CCAAGTTCGCGGCGCTTCCCGTCAAGCTTAATCGGGGCTCCCTTAAGGCTTCGAT 180
555 CCAAGTTCGCGGCGCTTCCCGTCAAGCTTAATCGGGGCTCCCTTAAGGCTTCGAT 496
181 TTATGCTTTTACCGGCACTTGACCCCAAAAATTGATGAGGTGATGATGATGATG 240
495 TTATGCTTTTACCGGCACTTGACCCCAAAAATTGATGAGGTGATGATGATGATG 436
241 GGCATGCGCCTGTATAGCGGCTTTCGCGCTTGAAGTGAAGTGAAGTGAAGTGA 300
435 GGCATGCGCCTGTATAGCGGCTTTCGCGCTTGAAGTGAAGTGAAGTGAAGTGA 376
301 GTGACCTCTTGTCCAACTGGAACAACACTCAACCTATCTCGTCTATTTTGATT 360
375 GTGACCTCTTGTCCAACTGGAACAACACTCAACCTATCTCGTCTATTTTGATT 316
361 TATTAAGGATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 420
315 TATTAAGGATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 256
421 TTAACGGGAATTTTAAACAAAATTTAAAGCTTAACATTTTCCATTCGCATTCAGGCTGC 479
255 TTAACGGGAATTTTAAACAAAATTTAAAGCTTAACATTTTCCATTCGCATTCAGGCTGC 196
480 GCAACTTGTGGAGAGCGGATCGGTGGGGGCTCTTTCGCTTAAAGCAGCGTGCAGAA 539
195 GCAACTTGTGGAGAGCGGATCGGTGGGGGCTCTTTCGCTTAAAGCAGCGTGCAGAA 136
540 GGGGATGTGTGCAAGGCGATTAAGTGGGTAACGCCAGGGTTTCCCAAGTCAAGAGTT 599
135 GGGGATGTGTGCAAGGCGATTAAGTGGGTAACGCCAGGGTTTCCCAAGTCAAGAGTT 76
600 GTTAAAGAGAGCGGCAAGGCGGCAATTAACCTCACTAAGAGGAA 646
75 GTTAAAGAGAGCGGCAAGGCGGCAATTAACCTCACTAAGAGGAA 29

RESULT 10
CB549906/c 702 bp mRNA linear EST 01-JUN-2003
LOCUS NMPL0007.B01 MMPL Macaca mulatta cDNA, mRNA sequence.
DEFINITION CB549906
ACCESSION CB549906
VERSION CB549906.1 GI:31299101
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopitheciinae; Macaca.
REFERENCE
1 (bases 1 to 702)
Katze,M.G., Bungartner,R., Korth,M., Feldman,R., Amjadi,M. and
Holzman,T.
Expressed sequence tags from Rhesus macaque placenta
JOURNAL Unpublished (2003)
COMMENT Contact: Holzman T
Katze Lab
University of Washington
Box 358070, Seattle, WA 98195-8070, USA
Tel: 206 732 6156
Fax: 206 732 6055
Email: ted@locke.hi.washington.edu
Similar to Genbank entry HS094592 U94592 Human uncoupling protein
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Plate: NMPL0007 row: B column: 01.
Location/Qualifiers
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Query Match 7.1%; Score 607.8; DB 6; Length 702;
Best Local Similarity 97.2%; Pred. No. 7.9e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

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61 CCGGTACACTTGGCAGGCGCCCTAGCGCGGCTCTTTCGCTTTCCTTCCTTCTCG 120
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121 CCAAGTTCGCGGCGCTTCCCGTCAAGCTTAATCGGGGCTCCCTTAAGGCTTCGAT 180
549 CCAAGTTCGCGGCGCTTCCCGTCAAGCTTAATCGGGGCTCCCTTAAGGCTTCGAT 490
181 TTATGCTTTTACCGGCACTTGACCCCAAAAATTGATGAGGTGATGATGATGATG 240
489 TTATGCTTTTACCGGCACTTGACCCCAAAAATTGATGAGGTGATGATGATGATG 430
241 GGCATGCGCCTGTATAGCGGCTTTCGCGCTTGAAGTGAAGTGAAGTGAAGTGA 300
429 GGCATGCGCCTGTATAGCGGCTTTCGCGCTTGAAGTGAAGTGAAGTGAAGTGA 370
301 GTGACCTCTTGTCCAACTGGAACAACACTCAACCTATCTCGGCTATTTTGATT 360
369 GTGACCTCTTGTCCAACTGGAACAACACTCAACCTATCTCGGCTATTTTGATT 310
421 TTAAGGGAATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 420
309 TTAAGGGAATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 250
421 TTAAGGGAATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 190
249 TTAAGGGAATTTTTCGCAATTTGCGCTATTTGTTAAAAATGAGCTGATTTAACAAAAT 190

Qy	480	GCACCTGTTGGGAAGGCGGATCGGTCGGGGCTCTTCGCTATTATTAAGCAGCGTGGGGAAG	539
Db	189	GCACTGTTGGGAAGGCGGATCGGTCGGGGCTCTTCGCTATTATTAAGCAGCGTGGGGAAG	130
Qy	540	GGGATGTGCTGCAGAGCGGATTAACTTGAGTAAAGCCAGGGTTTCCAGTCAGACGTT	599
Db	129	GGGGATGTGCTGCAGAGCGGATTAACTTGAGTAAAGCCAGGGTTTCCAGTCAGACGTT	70
Qy	600	GTAAGAAGACGGCGCATGAGCGGCAATTAAACCCCTACATAAAGGAA	646
Db	69	GTAAGAAGACGGCGCATGAGTATTGTAAATACACTCACTAATAGGCGAA	23
RESULT 11			
CB548528/c			
LOCUS			
DEFINITION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
SOURCE			
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Query Match			
Best Local Similarity 97.2%; Pred. No. 7.9e-172;			
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;			
Qy	1	CTGACGCGCCCTGTAGCGCGGCATTAAAGCGCGCGGCTGTGCTGTTACGCGCAGCGTGA	60
Db	702	CTGACGCGCCCTGTAGCGCGGCATTAAAGCGCGCGGCTGTGCTGTTACGCGCAGCGTGA	643
Qy	61	CCGCTACACTTGCACGCGCCCTTAGCGCCCGCTCTTTGCTTCTTCCTCTCTTCTCG	120
Db	642	CCGCTACACTTGCACGCGCCCTTAGCGCCCGCTCTTTGCTTCTTCCTCTCTTCTCG	583
Qy	121	CCAGCTTGCGCGGCTTTCGCCGTCAAGCTTAAATCGGCGGCTCCCTTAAGGTTCCGAT	180
Db	582	CCAGCTTGCGCGGCTTTCGCCGTCAAGCTTAAATCGGCGGCTCCCTTAAGGTTCCGAT	523
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Db	522	TTAGTGCTTTACGCGCAGCTTCGACCCCAAAAACTGATTAGGTGATGTTACAGTAGTG	463
Qy	241	GGCATTGCGCCCTGATAGACGGTTTTTGGCCCTTTAGCTTGAGTTCACGTTCTTTAATA	300

Db	462	GGCATTGCCCTGATAGACGGTTTTTTCGCCCTTTGAAGTTGAGAGTCCACGTTCTTTATA	403
Qy	301	GTGGAAGCTTTGTTCCAAAGCTGGAACAACTCAACCTATCTCGGCTATTTCTTTGATT	360
Db	402	GTGGAAGCTTTGTTCCAAAGCTGGAACAACTCAACCTATCTCGGCTATTTCTTTGATT	343
Qy	361	TATAAGGATTTTGGCCGATTTCCGCCCATTTGGTTAAATAATGAGCTGATTTAACAAAT	420
Db	342	TATAAGGATTTTGGCCGATTTCCGCCCATTTGGTTAAATAATGAGCTGATTTAACAAAT	283
Qy	421	TTAAGCGAATTTTAAACAAATATTTAAACGCTTCAATTTT-CCATTGCGCAATGAGCTGC	479
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Qy	540	GGGATGTGCTGCAAGGCGCATTTAAAGTTGGGTAAAGCGGATTTTCCAGCTCAAGAGTT	599
Db	162	GGGATGTGCTGCAAGGCGCATTTAAAGTTGGGTAAAGCGGATTTTCCAGCTCAAGAGTT	103
Qy	600	GTAAACGACGCGCAGTGAGCGGCGCATTTAAACCTCACTAAAGGAA	646
Db	102	GTAAACGACGCGCAGTGAGTTGTAATGCACTCAATATGAGGCGAA	56

RESULT 12

BO157858/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

SOURCE

BO157858 753 bp mRNA linear EST 24-APR-2002

NP103A09PL1P1067 phosphate starved leaf Medicago truncatula cDNA

clone NP103A09PL 5, mRNA sequence.

BO157858

BO157858.1 GI:20294915

EST.

Medicago truncatula (barrel medic)

Medicago truncatula

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.

1 (bases 1 to 753)

Lin, T., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W., May, G.D. and Harrison, M.J. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula phosphate-starved leaf library Unpublished (2000)

Contact: Harrison MJ

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7325

Fax: 580 221 7380

Email: mjharrison@noble.org

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Seq primer: TCACACGGAACACAGCTATGAC.

Location/Qualifiers

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/note="Vector: lambda Zap; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20mM potassium phosphate. RNA was prepared from above ground tissues."

ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 753;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 CTGACGCGCCCTGTAGCGGCGCATTTAAGCGCGGGGTGTGTGTGTACCGGACGCTGA 60
DB CTGACGCGCCCTGTAGCGGCGCATTTAAGCGCGGGGTGTGTGTGTACCGGACGCTGA 689
QY 61 CGGCTACACTTGCAGGCGCCCTGAGCGGCGCTCTTCTTCTTCTTCTTCTCTG 120
DB CGGCTACACTTGCAGGCGCCCTGAGCGGCGCTCTTCTTCTTCTTCTTCTCTG 629
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DB CCAAGTTCCGCGGCTTCCCGTCAAGCTTAATCGGCGGCTCCCTTTAGGGTCCGAT 569
QY 628 CCAAGTTCCGCGGCTTCCCGTCAAGCTTAATCGGCGGCTCCCTTTAGGGTCCGAT 569
DB 181 TTATGCTTTAGCGGACCTGACCCCAAAAATTGATGGGTGATGTTCAAGTGTG 240
QY 568 TTATGCTTTAGCGGACCTGACCCCAAAAATTGATGGGTGATGTTCAAGTGTG 509
DB 241 GGGCATCGCCCTATAGACGCTTTTTCGCGCTTGAAGCTTGACAGCTGCTTTAATA 300
QY 508 GGGCATCGCCCTATAGACGCTTTTTCGCGCTTGAAGCTTGACAGCTGCTTTAATA 449
DB 301 GTGAGCTCTGTTCGAACTGGAACAACCTCAACCTATCTGCTATTTTGTGAT 360
QY 448 GTGAGCTCTGTTCGAACTGGAACAACCTCAACCTATCTGCTATTTTGTGAT 389
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QY 328 TTAACGGGATTTTAAACAAATATTAACGCTTCAATTTTCCATGCGCTTCAAGCTG 269
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QY 268 GCAACTGTTGGGAAGGCGATCGGTGCGGCGCTTCTGCTATTAACGCACTGCGGAAG 209
DB 540 GGGGATGTGCTGCAAGCGATTAAGTTGGTTAACGCCAGGCTTTTCCAGTCAAGAGTT 599
QY 208 GGGGATGTGCTGCAAGCGATTAAGTTGGTTAACGCCAGGCTTTTCCAGTCAAGAGTT 149
QY 600 GTTAAACGAGCGGCGGATGAGCGGCGCAATTAACTCTCACTTAAAGGAA 646
DB 148 GTTAAACGAGCGGCGGATGAGCGGCGCAATTAACTCTCACTTAAAGGAA 102

RESULT 13
B0158943/c 758 bp mRNA linear EST 24-APR-2002
LOCUS NF095D07P.LF1060 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION clone NF095D07P.L 5', mRNA sequence.
B0158943
ACCESSION B0158943
VERSION B0158943.1 GI:20256000
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 758)

REFERENCE
AUTHORS Liu J., Scott A.D., Harris A.R., Gonzales R.A., Bell C.J.,
Flores H.R., Imman J.T., Weller J.W., May G.D. and Harrison M.J.
TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation
JOURNAL Medicago truncatula phosphate-starved leaf library
COMMENT Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division

The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7380
Email: mjharrison@noble.org
Insert Length: 758 Std Error: 0.00
Plate: 095 row: D column: 07
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Location/Qualifiers
1. 758

FEATURES

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/issue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap. At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, the plants were fertilized twice weekly with 1/2 Hoaglands solution containing only 20mM potassium phosphate. RNA was prepared from above ground tissues."

ORIGIN

Query Match 7.1%; Score 607.8; DB 5; Length 758;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 CTGACGCGCCCTGTAGCGGCGCATTTAAGCGCGGGGTGTGTGTGTACCGGACGCTGA 60
DB 747 CTGACGCGCCCTGTAGCGGCGCATTTAAGCGCGGGGTGTGTGTGTACCGGACGCTGA 688
QY 61 CGGCTACACTTGCAGGCGCCCTGAGCGGCGCTCTTCTTCTTCTTCTTCTCTG 120
DB CGGCTACACTTGCAGGCGCCCTGAGCGGCGCTCTTCTTCTTCTTCTTCTCTG 628
QY 687 CGGCTACACTTGCAGGCGCCCTGAGCGGCGCTCTTCTTCTTCTTCTTCTCTG 628
DB 121 CCAAGTTCCGCGGCTTCCCGTCAAGCTTAAATCGGCGGCTCCCTTTAGGGTCCGAT 180
QY 627 CCAAGTTCCGCGGCTTCCCGTCAAGCTTAAATCGGCGGCTCCCTTTAGGGTCCGAT 568
DB 181 TTATGCTTTAGCGGACCTGACCCCAAAAATTGATGGGTGATGTTCAAGTGTG 240
QY 567 TTATGCTTTAGCGGACCTGACCCCAAAAATTGATGGGTGATGTTCAAGTGTG 508
DB 241 GGGCATCGCCCTATAGACGCTTTTTCGCGCTTGAAGCTTGACAGCTGCTTTAATA 300
QY 507 GGGCATCGCCCTATAGACGCTTTTTCGCGCTTGAAGCTTGACAGCTGCTTTAATA 448
DB 301 GTGAGCTCTGTTCGAACTGGAACAACCTCAACCTATCTGCTATTTTGTGAT 360
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DB 540 GGGGATGTGCTGCAAGCGATTAAGTTGGTTAACGCCAGGCTTTTCCAGTCAAGAGTT 599
QY 207 GGGGATGTGCTGCAAGCGATTAAGTTGGTTAACGCCAGGCTTTTCCAGTCAAGAGTT 148
QY 600 GTTAAACGAGCGGCGGATGAGCGGCGCAATTAACTCTCACTTAAAGGAA 646
DB 147 GTTAAACGAGCGGCGGATGAGCGGCGCAATTAACTCACTTAAAGGAA 101

RESULT 14
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LOCUS NF070607LP1061 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION clone NF070607LP 5', mRNA sequence.
ACCESSION BQ158750
VERSION BQ158750.1 GI:20295807
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 764)
Lin, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7320
Email: mjharrison@noble.org
Insert Length: 764 Std Error: 0.00
Plate: 070 row: F column: 07
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Location/Qualifiers
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/tissue_type="leaf"
/dev_stage="trifoliolate"
/note="Vector: Lambda Zap; At the trifoliolate stage, M.
truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN
Query Match 7.1%; Score 607.8; DB 5; Length 764;
Best Local Similarity 97.2%; Pred. No. 8.1e-172;
Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1 CTGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTTAGCGCGAGGTGA 60
DB 748 CTGACGCGCCCTGTAGCGCGCATTAAGCGCGCGGTGTGTTAGCGCGAGGTGA 689
QY 61 CGGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCCTTTCCTTTCCTTTCG 120
DB 688 CGGCTACACTTGGCAGCGCCCTAGCGCCGCTCTTTCCTTTCCTTTCCTTTCG 629
QY 121 CCAGCTTGGCGCGCTTCCCGCTCAAGCTTAATGCGGGGCTCCCTTTAGGTTCCGAT 180
DB 628 CCAAGTTGGCGCGCTTCCCGCTCAAGCTTAATGCGGGGCTCCCTTTAGGTTCCGAT 569
QY 181 TTAGTGCTTTAGCGGCACTGACCCCAAAAATTGATTAGGTTGATGATGATGATG 240
DB 566 TTAGTGCTTTAGCGGCACTGACCCCAAAAATTGATTAGGTTGATGATGATGATG 509
QY 241 GGGCATCGCCCTGATGACGCTTTTTCGCTTTGAGTTGAGTTGACGTTCTTTAATA 300
DB 508 GGGCATCGCCCTGATGACGCTTTTTCGCTTTGAGTTGAGTTGACGTTCTTTAATA 449
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QY 421 TTAACGCGAATTTTAAACAAATATTTAAGCTTACGAATTT-CAATTGGCCATTCAAGCTGC 479
DB 328 TTAACGCGAATTTTAAACAAATATTTAAGCTTACGAATTTGGCCATTTCAGGCTGC 269
QY 480 GCAACTGTTGGAGAGGCGGATCGTGCGGCTCTTTCCTATTATTAAGCGCAGTGGGAAAG 539
DB 268 GCAACTGTTGGAGAGGCGGATCGTGCGGCTCTTTCCTATTATTAAGCGCAGTGGGAAAG 209
QY 540 GGGAGATGCTGCAAGGCGGATTAATTGGGTAAACCCAGGTTTCCCATGACAGCTT 599
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RESULT 15
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LOCUS NF070606PL1F1050 Phosphate starved leaf Medicago truncatula cDNA
DEFINITION clone NF070606PL 5', mRNA sequence.
ACCESSION BQ158875
VERSION BQ158875.1 GI:20295932
KEYWORDS EST.
SOURCE Medicago truncatula (barrel medic)
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliaceae;
Medicago.
1 (bases 1 to 771)
Lin, J., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J.,
Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Harrison, M.J.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula phosphate-starved leaf library
Unpublished (2000)
Contact: Harrison MJ
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7325
Fax: 580 221 7320
Email: mjharrison@noble.org
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truncatula plants were transplanted to phosphate-free sand
and grown for a further 30 days. During this 30 day
period, the plants were fertilized twice weekly with 1/2
Hoaglands solution containing only 20uM potassium
phosphate. RNA was prepared from above ground tissues."

ORIGIN
Query Match 7.1%; Score 607.8; DB 5; Length 771;
Best Local Similarity 97.2%; Pred. No. 8.2e-172;

Matches 629; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1 CTGACGGCCCTGTAGCGGCGCATTTAAGCGGCGGCTGTGTGTACGCGCAGCGTGA 60
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Db 750 CTGACGGCCCTGTAGCGGCGCATTTAAGCGGCGGCTGTGTGTACGCGCAGCGTGA 691
|
QY 61 CCGGTACACTTGTCCAGCGCCCTAAGCGCCCGCTTCTTCTTCTTCTTCTG 120
|
Db 690 CCGGTACACTTGTCCAGCGCCCTAAGCGCCCGCTTCTTCTTCTTCTTCTG 631
|
QY 121 CCAAGTTGCGGGCTTCCCGTCAAGCTTAAATGGGGGCTCCCTTAGGGTCCGAT 180
|
Db 630 CCAAGTTGCGGGCTTCCCGTCAAGCTTAAATGGGGGCTCCCTTAGGGTCCGAT 571
|
QY 181 TTAGTCTTACGGCAGCTCGACCCCAAAAACTTGATTAGGGTATGTTCAGTATG 240
|
Db 570 TTAGTCTTACGGCAGCTCGACCCCAAAAACTTGATTAGGGTATGTTCAGTATG 511
|
QY 241 GGCCTATGCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGAGTCCACGTTCTTAATA 300
|
Db 510 GGCCTATGCGCCCTGATAGCGGTTTTTGGCCCTTTGACGTTGAGTCCACGTTCTTAATA 451
|
QY 301 GTGACTCTTGTCCAACTGGAAACAACACTCAACCTATCTGGTCTATTTCTTGATT 360
|
Db 450 GTGACTCTTGTCCAACTGGAAACAACACTCAACCTATCTGGTCTATTTCTTGATT 391
|
QY 361 TATAGGGATTTTGGCGCTATTTGGCTATTTGTTAAAAATGAGCTGATTTACAAAAT 420
|
Db 390 TATAGGGATTTTGGCGCTATTTGGCTATTTGTTAAAAATGAGCTGATTTACAAAAT 331
|
QY 421 TTAACGGAAATTTTACAAAATTTAACGCTTACAAATT-CCATTGCGCAATTCAGGCTGC 479
|
Db 330 TTAACGGAAATTTTACAAAATTTAACGCTTACAAATTGCGCAATTCAGGCTGC 271
|
QY 480 GCAACTGTGGGAAGGCGCATCGTGGGGCTCTTGCTATTACGCCAGCTGGCGAAAG 539
|
Db 270 GCAACTGTGGGAAGGCGCATCGTGGGGCTCTTGCTATTACGCCAGCTGGCGAAAG 211
|
QY 540 GGGGATGTGCTGCAAGGCGATTAGTTGGGTAAAGCCAGGGTTTTCCCAAGTCAAGAGTT 599
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Db 210 GGGGATGTGCTGCAAGGCGATTAGTTGGGTAAAGCCAGGGTTTTCCCAAGTCAAGAGTT 151
|
QY 600 GTAAAAAGAGCGCCAGTGAAGCGCGCAATTAAACCTCACTAAAGGAA 646
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Db 150 GTAAAAAGAGCGCCAGTGAATTTGTAATACGACTCACTATAGGCGAA 104
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Search completed: March 23, 2005, 17:05:35
Job time : 16279 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model .

Run on: March 23, 2005, 08:17:54 ; Search time 2688 Seconds
(without alignments)
18805.309 Million cell updates/sec

Title: US-09-275-883-1_COPY_1_8539
Perfect score: 8539
Sequence: 1 ctgacgcgcctcgtacgcgc.....atactacacaccaccact 8539

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: geneseqn1980s:*\n2: geneseqn1990s:*\n3: geneseqn2000s:*\n4: geneseqn2001as:*\n5: geneseqn2001bs:*\n6: geneseqn2002as:*\n7: geneseqn2002bs:*\n8: geneseqn2003as:*\n9: geneseqn2003bs:*\n10: geneseqn2003cs:*\n11: geneseqn2003ds:*\n12: geneseqn2004as:*\n13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8539	100.0	11282	2	AA227850 Complete
2	8539	100.0	11282	4	AAD04741 Alphavira
3	8539	100.0	11282	5	AAF84024 Complete
4	8539	100.0	11282	12	ADL71889 Temperatu
5	7657.2	89.7	12068	12	ADL71890 Temperatu
6	7657.2	89.7	12068	12	ADL71890 Temperatu
7	7657.2	89.7	12068	12	ADL71890 Temperatu
8	7657.2	89.7	12068	12	ADL71890 Temperatu
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17	7657.2	89.7	12068	12	ADL71890 Temperatu
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19	7657.2	89.7	12068	12	ADL71890 Temperatu
20	7657.2	89.7	12068	12	ADL71890 Temperatu

21	7634.8	89.4	11703	13	AD67767 Sindbis v
22	7634.8	89.4	11740	8	ABX81526 Sindbis v
23	7634.8	89.4	11740	9	ADA50626 Sindbis v
24	7634.2	89.4	16847	12	AD007464 Japanese
25	7632.6	89.4	11927	2	AAV77356 Polynucle
26	7632.6	89.4	11927	3	AAA90388 Plasmid p
27	7623.6	89.3	11703	3	AAC64506 Alphaviru
28	7620.4	89.2	11703	3	AAC64507 Alphaviru
29	7618.8	89.2	11703	3	AAV33476 Sindbis v
30	7617.2	89.2	8000	2	AAV59321 Sindbis v
31	7617.2	89.2	8000	2	AAV58571 Sindbis v
32	7617.2	89.2	8000	8	ABX81524 Sindbis v
33	7617.2	89.2	8000	9	ADA50624 SIN-1 vir
34	7612.4	89.1	16656	2	AAQ86154 Eukaryoti
35	7612.4	89.1	16656	2	AAV42364 Represent
36	7612.4	89.1	16656	2	AAV60125 Represent
37	7612.4	89.1	16656	2	AAV70684 Represent
38	7612.4	89.1	16656	3	AAZ92892 Represent
39	7612.4	89.1	16656	3	AAZ92765 Represent
40	7612.4	89.1	16656	6	AAI38772 DNA of eu
41	7612.4	89.1	16656	12	AD130344 Eukaryoti
42	7610.8	89.1	16656	6	ABK46238 Eukaryoti
43	7602.8	89.0	16656	2	AAT30787 Alphaviru
44	7598.8	89.0	16958	8	AAI55269 DNA of ex
45	7457	87.3	11687	6	AAD25136 Sinchiron

ALIGNMENTS

RESULT 1
ID AA227850 standard; cDNA; 11282 BP.
XX
AC AA227850:
XX
DT 23-DEC-1999 (first entry)
XX
DE Complete cDNA sequence of PCYTTs.
XX
KW Gene expression system; cis-acting element; gene therapy;
KW Temperature-sensitive RNA-dependent RNA polymerase;
KW Inducible alphavirus gene expression system; PCYTTs;
KW hormone-based gene control system; tetracycline gene control system; ss.
XX
OS Synthetic.
XX
PN WO9950432-A1.
XX
PD 07-OCT-1999.
XX
PE 25-MAR-1999; 99WO-IB000523.
XX
PR 27-MAR-1998; 98US-0079562P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PA (RENN/) RENNER W A.
XX
PA (NIEB/) NIEBA L.
XX
PA (BOOR/) BOORSMA M.
XX
PI Renner WA, Nieba L, Boorsma M;
XX
DR WPI; 1999-591327/50.
XX
FT A new system to regulate gene expression in eukaryotic cells.
XX
PS Claim 15; Fig 3; 99p; English.
XX
CC This sequence represents the complete cDNA sequence for the vector
CC pCYTTs. The invention relates to a DNA molecule comprising a
CC polynucleotide (I) encoding an RNA molecule. The encoded RNA comprises:
CC (a) at least one cis-acting element; (b) an open reading frame (ORF1)
CC encoding a non-cytopathic, temperature-sensitive RNA-dependent RNA

CC polymerase; and (c) a second sequence that is: (i) a protein-encoding ORF
CC (ORF2) that is in a translatable format after RNA-dependent RNA
CC replication event(s); (ii) a sequence complementary to the ORF2; or (iii)
CC a sequence encoding an untranslated RNA molecule. The polypeptide sequence is
CC an example of the DNA molecule, and is an inducible alpha-viral gene
CC expression system. The invention is used in gene therapy and recombinant
CC technology to regulate expression of introduced genes. The invention does
CC not have the problems of toxicity and/or high basal level expression
CC associated with prior art tetracycline-based and hormone-based gene
CC control systems
XX
SQ Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 2; Length 11282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8539; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTGACGGCCCTGATAGGGGGGCGCATTAAGCGGGGGGTGTGTGTATACCGCAGCTGA 60
DB 1 CTGACGGCCCTGATAGGGGGGCGCATTAAGCGGGGGGTGTGTGTATACCGCAGCTGA 60
QY 61 CCGGTACACTTCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCTTCTTCTTCTG 120
DB 61 CCGGTACACTTCCAGCGCCCTAGCGCCGCTCTTTCGCTTCTTCTTCTTCTTCTG 120
QY 121 CCACGTTCCGCGGCTTTCCCGCTCAAGCTTAAATCGGGGGCTTCCCTTAAGGTTCCGAT 180
DB 121 CCACGTTCCGCGGCTTTCCCGCTCAAGCTTAAATCGGGGGCTTCCCTTAAGGTTCCGAT 180
QY 181 TTATGCTTTTACCGGACCTGAGACCCCAAAAACCTGATTTAGGGGATAGTTTCAAGTGTG 240
DB 181 TTATGCTTTTACCGGACCTGAGACCCCAAAAACCTGATTTAGGGGATAGTTTCAAGTGTG 240
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DB 241 GGGCATGCGCCCTGATAGCGGTTTTCGCGCTTGAAGTGTGAGTCCACGCTTTTATA 300
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DB 301 GTGACCTTCTTGTTCAAACTGGAACAACCTCAACCTATCTGCTATCTTTTGAT 360
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DB 361 TATAAGGATTTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCGCTTTCGCG 420
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DB 421 TTAACGGAAATTTTAAACAAATATTTAAGCTTCAATTTCCATTTCCAGTTCAGGCTG 480
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QY 541 GGGATGTCGCAAGGCGGATTAAGTTGGATAGCGCGGCTTTCGCGACGTGCGAAAG 600
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DB 661 TGAATCCAGTCTTATGCAATCTTGTATCTTTGCAACATGTTAAGATGATGCA 720
QY 721 CATGCTTAAAGAGAGAAAGCAACCGTCAATGCGGATTTGGAGAGTAAAGTGTAC 780
DB 721 CATGCTTAAAGAGAGAAAGCAACCGTCAATGCGGATTTGGAGAGTAAAGTGTAC 780
QY 781 GATCGCTTATTAAGAGCAACAGCGGCTTGAATGATGATGATGATGATGATGATGAT 840
DB 781 GATCGCTTATTAAGAGCAACAGCGGCTTGAATGATGATGATGATGATGATGATGAT 840

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DB 841 TTCGCGATTCAGAGATATTTGATTTAAGTGCCTCACTCGATACCGTGAATGACGG 900
QY 901 CCGATGACACACTTATTTGAATCAACAGCGGACCAATTTGACATTCATCAATGAGAA 960
DB 901 CCGATGACACACTTATTTGAATCAACAGCGGACCAATTTGACATTCATCAATGAGAA 960
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DB 1621 GGAATAATGCTGATATAGAGAGAGAGTGAAGCCGGGCTCCGGGTTATTTCTCC 1680
QY 1681 GTAGATGACACTTATTCAGAAACAGAGGCACTTTCAGAGCTGCGATCTTCATG 1740
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DB 1861 TACGCGGTTTACACAAATAGCAGAGGCTTCTTGTATGCAAAAGTTACTGACACATGAAA 1920
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[illegible]

Db	3001	AAGGAAGAAGCCTCAGGCTGTGTCTCTCGGAGAACTGACACAACTCCTCTATCATGAG	3068
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Db	3061	CTAGCTCTGAGGGAGCTGAAGACCCGACCTGCGGTCCCGTACAAAGTCCAAACATTAAGA	3120
Qy	3121	GTGATAGGCACACCGGGGTCCGGGCAATCAGCTATTATCAAGTCAACTGTCACGGACGA	3180
Db	3121	GTGATAGGCACACCGGGGTCCGGGCAATCAGCTATTATCAAGTCAACTGTCACGGACGA	3180
Qy	3181	GATCTTGTTCACGACGGAAAGAAAGAAATTTGTGCGAAATTTGAGGCGCAGTCTAAGA	3240
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Qy	3241	CTGAGGGGTATGACAGATTACGTGCAAGACAGTAGATTCCGTTATGCTCAACGATGCCAC	3300
Db	3241	CTGAGGGGTATGACAGATTACGTGCAAGACAGTAGATTCCGTTATGCTCAACGATGCCAC	3300
Qy	3301	AAAGCCGTGAAGATGCTGTACGTTGACGAGACGCTTCCGCTGCCACGCAAGAGCACTACTT	3360
Db	3301	AAAGCCGTGAAGATGCTGTGTACGTTGACGAGACGCTTCCGCTGCCACGCAAGAGCACTACTT	3360
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Db	3361	GCGTTGATGTGATATCGTCAAGCCCCGCAAGAAAGTAGATCTATGCGGAGACCCCATGCAA	3420
Qy	3421	TGCGGATTCCTTCAACATGATGCAACTAAAGGTACATTTTCATCACTCCCTGAAGAAAGACATA	3480
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Qy	3481	TGCACCAAGACATTTCTACAGTATATCTCCCGCGTTGCACACAGCCAGTTACAGCTATT	3540
Db	3481	TGCACCAAGACATTTCTACAGTATATCTCCCGCGTTGCACACAGCCAGTTACAGCTATT	3540
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Qy	3601	GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTTGACATGTTTC	3660
Db	3601	GAAATCGATATTACAGGGGCCACAAAGCCGAAGCCAGGGGATATCATCTTGACATGTTTC	3660
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Qy	3781	CCACTGTACGGGATCATCATGAGACATGTGAACGTGTGCTCACCCGCACTGABAGACAG	3840
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Qy	4081	GAACTGTTTCCCAACAGTGTGGGATGACAAACCACTTCCGCAATTTACGCTTATGACGTA	4140
Db	4081	GAACTGTTTCCCAACAGTGTGGGATGACAAACCACTTCCGCAATTTACGCTTATGACGTA	4140

QY 4141 ATTGCAATTAAAGTTTTCGGATGGAAGTGAAGAAGGACGTTTCTTAAACAGAGCATC 4200
DB 4141 ATTGCAATTAAAGTTTTCGGATGGAAGTGAAGAAGGACGTTTCTTAAACAGAGCATC 4200
QY 4201 CCATTAACGTACATCCCGCGGATTCAGCGAGGCGGTAGTCTATTGGACAAAGCCCA 4260
DB 4201 CCATTAACGTACATCCCGCGGATTCAGCGAGGCGGTAGTCTATTGGACAAAGCCCA 4260
QY 4261 GGAACCCGCAAGTATGGGTACATCAGCGCATTCGCCCGGAATCTCCCGTAGATTCCG 4320
DB 4261 GGAACCCGCAAGTATGGGTACATCAGCGCATTCGCCCGGAATCTCCCGTAGATTCCG 4320
QY 4321 GTGTTCCAGCTAGCTGGGAAGGCAACAACCTTGATTTGACAGCGGGAAGAACAGATT 4380
DB 4321 GTGTTCCAGCTAGCTGGGAAGGCAACAACCTTGATTTGACAGCGGGAAGAACAGATT 4380
QY 4381 ATCTGTGACAGCAATTAACCTGTGTCGGTGAACCGGCAATCTTCTCAAGCTTAGTCCC 4440
DB 4381 ATCTGTGACAGCAATTAACCTGTGTCGGTGAACCGGCAATCTTCTCAAGCTTAGTCCC 4440
QY 4441 GAGTACAAAGAGAAACAACCCGCGCTCAAAAAATTTCTTGAACAGTTCAAAACACAC 4500
DB 4441 GAGTACAAAGAGAAACAACCCGCGCTCAAAAAATTTCTTGAACAGTTCAAAACACAC 4500
QY 4501 TCAATCTTGTGTGATCAAGAGAAAAATTGAAGCTCCCGTAAGAGAAATCGAATGATC 4560
DB 4501 TCAATCTTGTGTGATCAAGAGAAAAATTGAAGCTCCCGTAAGAGAAATCGAATGATC 4560
QY 4561 GCCCGCAATGGCAGACGCGGTGAGATTAAGAACTAACCTGGCTTCGGGTTTCCGCG 4620
DB 4561 GCCCGCAATGGCAGACGCGGTGAGATTAAGAACTAACCTGGCTTCGGGTTTCCGCG 4620
QY 4621 CAGGCAAGTACGACCTGTGTTCATCAACATTTGAATTAATAACAGAAACCAACTTT 4680
DB 4621 CAGGCAAGTACGACCTGTGTTCATCAACATTTGAATTAATAACAGAAACCAACTTT 4680
QY 4681 CAGGAGTGGCAAGCAATTCGGGCGAATTAAACCTTTTCGGGTTTCCGCG 4740
DB 4681 CAGGAGTGGCAAGCAATTCGGGCGAATTAAACCTTTTCGGGTTTCCGCG 4740
QY 4741 TTAAATCAGAGGACACCTGTGTGAGATTCATAGGCTAACGCGGCAACAGTGA 4800
DB 4741 TTAAATCAGAGGACACCTGTGTGAGATTCATAGGCTAACGCGGCAACAGTGA 4800
QY 4801 GAGCTAGTCAACGCTCTTGCAGAAAGTTGTCAAGGTTGTGAGGAGAACAGATTGT 4860
DB 4801 GAGCTAGTCAACGCTCTTGCAGAAAGTTGTCAAGGTTGTGAGGAGAACAGATTGT 4860
QY 4861 GTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGCAACAGCGTACAG 4920
DB 4861 GTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGCAACAGCGTACAG 4920
QY 4921 CAATTCAACCCGCAACATCTGATTTGCTGATTTTCCGATGAGGATGAGAT 4980
DB 4921 CAATTCAACCCGCAACATCTGATTTGCTGATTTTCCGATGAGGATGAGAT 4980
QY 4981 GGAAGTGGAGCCGCGGTATACCGGCAAAAAAGGAGAAATATGCTGACGTCAAGAG 5040
DB 4981 GGAAGTGGAGCCGCGGTATACCGGCAAAAAAGGAGAAATATGCTGACGTCAAGAG 5040
QY 5041 GAAAGCAATTTGCAACGAGCAATCCCTGGTGAACAGGCAAGAGTCTCCGCGGC 5100
DB 5041 GAAAGCAATTTGCAACGAGCAATCCCTGGTGAACAGGCAAGAGTCTCCGCGGC 5100
QY 5101 ATCTATAAGCTTGGCGGACGAGTTTACCGATTACGCGACGAGGACGCGCAAG 5160
DB 5101 ATCTATAAGCTTGGCGGACGAGTTTACCGATTACGCGACGAGGACGCGCAAG 5160
QY 5161 ATGACGTGTGTCTAGGAAAGAAAGTATCAGCGGTCGCGCTGATTTCCGAAAGCAC 5220
DB 5161 ATGACGTGTGTCTAGGAAAGAAAGTATCAGCGGTCGCGCTGATTTCCGAAAGCAC 5220

QY 5221 CCAGAGCAGAACCTTGAATTTGCTACAAAGCGCTTACATGACAGTGGCAGACTTAGTA 5280
DB 5221 CCAGAGCAGAACCTTGAATTTGCTACAAAGCGCTTACATGACAGTGGCAGACTTAGTA 5280
QY 5281 AATGAACATTAATCAAGTGTGTGCTGCTTCCATCTCTATCTACAGGCAATTAACGACGC 5340
DB 5281 AATGAACATTAATCAAGTGTGTGCTGCTTCCATCTCTATCTACAGGCAATTAACGACGC 5340
QY 5341 GGAAGAGCCGCTTGAATATCACTTAATCTGCTTGAACAACCGGCTTACAGAACTGAC 5400
DB 5341 GGAAGAGCCGCTTGAATATCACTTAATCTGCTTGAACAACCGGCTTACAGAACTGAC 5400
QY 5401 GCGGAGTAAACCATCTATTGCTTGAATGAAGAGTGAAGAAATGACGCGGCACTC 5460
DB 5401 GCGGAGTAAACCATCTATTGCTTGAATGAAGAGTGAAGAAATGACGCGGCACTC 5460
QY 5461 CAATTAAGAGTCTGTAAACAGTGTGAAGATGAAGATATGAGATTCGACATGAGTTA 5520
DB 5461 CAATTAAGAGTCTGTAAACAGTGTGAAGATGAAGATATGAGATTCGACATGAGTTA 5520
QY 5521 GTATGATTCATTCAGACAGTTGCTTGAAGGAGAAAGGATTCAGTACTACAAAGGA 5580
DB 5521 GTATGATTCATTCAGACAGTTGCTTGAAGGAGAAAGGATTCAGTACTACAAAGGA 5580
QY 5581 AATGTATTCGTAATTCGTAAGGACCAAAATTCATCAAGCAGCAAAAGACATGCGGAG 5640
DB 5581 AATGTATTCGTAATTCGTAAGGACCAAAATTCATCAAGCAGCAAAAGACATGCGGAG 5640
QY 5641 ATTAAGGTCCTGTGCTTGAATGAACAGGAAATTAATGAACAATGCTGTGCTTACATTTG 5700
DB 5641 ATTAAGGTCCTGTGCTTGAATGAACAGGAAATTAATGAACAATGCTGTGCTTACATTTG 5700
QY 5701 GGTGAGACCATGGAAGCAATCCGCGAAAGTCCCGGTGACCAATTAACCGTGTGTAC 5760
DB 5701 GGTGAGACCATGGAAGCAATCCGCGAAAGTCCCGGTGACCAATTAACCGTGTGTAC 5760
QY 5761 CCGCCAAAACCTTCCGCTGCTTGTGATGATATGCCATGACCGAAGGCTCCACAGA 5820
DB 5761 CCGCCAAAACCTTCCGCTGCTTGTGATGATATGCCATGACCGAAGGCTCCACAGA 5820
QY 5821 CTTAAGAGCAATTAAGTCAAGAAAGTTACAGATGCTCTCAACCCCTTCTTAAGAC 5880
DB 5821 CTTAAGAGCAATTAAGTCAAGAAAGTTACAGATGCTCTCAACCCCTTCTTAAGAC 5880
QY 5881 AAAATTAAGAAATGTCAGAAAGTTCAGTGCAGAAAGTATGCTGTATTATCCGACACT 5940
DB 5881 AAAATTAAGAAATGTCAGAAAGTTCAGTGCAGAAAGTATGCTGTATTATCCGACACT 5940
QY 5941 CCGCATTGCTTCCGCGCTGATGATGATGAAGATGCCAGAAACAGCTTACCGCTCTCT 6000
DB 5941 CCGCATTGCTTCCGCGCTGATGATGATGAAGATGCCAGAAACAGCTTACCGCTCTCT 6000
QY 6001 GCACAGGCGGAGAGGCGCCGGAAGTGTAGGAGACAGCTGCACTTACAGCTGATAC 6060
DB 6001 GCACAGGCGGAGAGGCGCCGGAAGTGTAGGAGACAGCTGCACTTACAGCTGATAC 6060
QY 6061 ACCTGCTTATGATGACAGACATCTCACTGATATGATGACAGTACGAGAGGCTCACTT 6120
DB 6061 ACCTGCTTATGATGACAGACATCTCACTGATATGATGACAGTACGAGAGGCTCACTT 6120
QY 6121 TTTTGAAGCTTTAGGAGATCGGACAACTCTATTACTAGTATGACAGATTGTGTCAGGA 6180
DB 6121 TTTTGAAGCTTTAGGAGATCGGACAACTCTATTACTAGTATGACAGATTGTGTCAGGA 6180
QY 6181 CCTAGTTCACTAGAGATGTAGAACGGAAGGAGGTGTGAGGCTGATGCGTTCATGCGCTC 6240
DB 6181 CCTAGTTCACTAGAGATGTAGAACGGAAGGAGGTGTGAGGCTGATGCGTTCATGCGCTC 6240
QY 6241 CAAAGCCTGCGCTTATTCACCGCAAGGCTTAAAGAAAGTGGCCGCTTGCAGCGGCA 6300
DB 6241 CAAAGCCTGCGCTTATTCACCGCAAGGCTTAAAGAAAGTGGCCGCTTGCAGCGGCA 6300
QY 6301 AGAAAAGAGCCCATCTCAACCGGCAAGCAATAGCTGTGAGTCCCTCACTCTTTTGTGT 6360

[illegible]

Db	7381	GCTGGGAAGCCAAATTAGATTACCACTGAGTTTGTACCCGCATATGTAGCTAGACTGAAA	7440
Qy	7441	GGCCCTTAAGCCGCGCGCACTATTTTGGCAAGAAGCGTATATTTGGTCCCATTTGCCAAGAGTGT	7500
Db	7441	GGCCCTTAAGCCGCGCGCACTATTTTGGCAAGAAGCGTATATTTGGTCCCATTTGCCAAGAGTGT	7500
Qy	7501	CCTATGTGATAGATTTCGTATCTGATGGAACATGAAAAAGAGACGTGAAGTTTACACCAAGGACGAAA	7560
Db	7501	CCTATGTGATAGATTTCGTATCTGATGGAACATGAAAAAGAGACGTGAAGTTTACACCAAGGACGAAA	7560
Qy	7561	CACACAGAAAGAAACCCGAAAGTACAAAGTGTAACAGCCGCAAGAACCCCTGGCGACTGCT	7620
Db	7561	CACACAGAAAGAAACCCGAAAGTACAAAGTGTAACAGCCGCAAGAACCCCTGGCGACTGCT	7620
Qy	7621	TACTTATGCGGGATTCTACCCGGGAATTAGTGCGTAGGCTTACCGCGCTTCTTCCAAAC	7680
Db	7621	TACTTATGCGGGATTCTACCCGGGAATTAGTGCGTAGGCTTACCGCGCTTCTTCCAAAC	7680
Qy	7681	ATTCAACACGCTTTTGGATGTCCGCGGAGGATTTTGAATGCAATCATAGCAACAATTCC	7740
Db	7681	ATTCAACACGCTTTTGGATGTCCGCGGAGGATTTTGAATGCAATCATAGCAACAATTCC	7740
Qy	7741	AAGCAAGGCGACCCGGGTACTGGGAGACGGATATGCGATCATTCGACAAAGCGAAGACGAC	7800
Db	7741	AAGCAAGGCGACCCGGGTACTGGGAGACGGATATGCGATCATTCGACAAAGCGAAGACGAC	7800
Qy	7801	GCTATGGCGTTAACCGGCTGTGATGATCTTGGAGAGACCTGGGTGTGATTCACACACTATCTC	7860
Db	7801	GCTATGGCGTTAACCGGCTGTGATGATCTTGGAGAGACCTGGGTGTGATTCACACACTATCTC	7860
Qy	7861	GACTTGTATCGAGTGGCTTTGGAGAAATATCATCCACCATTCTACCGGTTACTGCT	7920
Db	7861	GACTTGTATCGAGTGGCTTTGGAGAAATATCATCCACCATTCTACCGGTTACTGCT	7920
Qy	7921	TTTAAATTCGGGGGGAGTAGTAATAATCCGGAAATGTTTCCACACTTTTGTCAACAAGTT	7980
Db	7921	TTTAAATTCGGGGGGAGTAGTAATAATCCGGAAATGTTTCCACACTTTTGTCAACAAGTT	7980
Qy	7981	TTGAATGTCGTTATCGCAGCAGAGTACTAAGAAAGCGGCTTTAAACGTCAGATGTGCA	8040
Db	7981	TTGAATGTCGTTATCGCAGCAGAGTACTAAGAAAGCGGCTTTAAACGTCAGATGTGCA	8040
Qy	8041	GCGTTTATGGCGACGACAAACATCATACATGAGTAGATCTGCAAAAGAAATGGCTGAG	8100
Db	8041	GCGTTTATGGCGACGACAAACATCATACATGAGTAGATCTGCAAAAGAAATGGCTGAG	8100
Qy	8101	AGGTGCGGCACTGCGCTCAACATGGAAGTTAAGTATCATCGACGAGTATCGGTGAAGAGA	8160
Db	8101	AGGTGCGGCACTGCGCTCAACATGGAAGTTAAGTATCATCGACGAGTATCGGTGAAGAGA	8160
Qy	8161	COACCTTACTCTGCGGGGGAGTTTATCTGTGCAAAATTCGGTTACTTCCACACGCTGCGC	8220
Db	8161	COACCTTACTCTGCGGGGGAGTTTATCTGTGCAAAATTCGGTTACTTCCACACGCTGCGC	8220
Qy	8221	GTGGCGGATCCCTGAAAAGGCTGTTAAAGTTGGGTAAACCGCTCCAGCCGACGACGAG	8280
Db	8221	GTGGCGGATCCCTGAAAAGGCTGTTAAAGTTGGGTAAACCGCTCCAGCCGACGACGAG	8280
Qy	8281	CAAGCGAAGACAGAAAGACGCGCTCTGTGATATAAACAAAGGGGTGGTTTAAAGTGTGT	8340
Db	8281	CAAGCGAAGACAGAAAGACGCGCTCTGTGATATAAACAAAGGGGTGGTTTAAAGTGTGT	8340
Qy	8341	ATAACAGGCACTTTAGCAGGTGCGGTGACGACCGGGATGAGGTAGACAAATATTAACAACCT	8400
Db	8341	ATAACAGGCACTTTAGCAGGTGCGGTGACGACCGGGATGAGGTAGACAAATATTAACAACCT	8400
Qy	8401	GTCTTACTGCAATTGAGAACTTTTGCCAGAGCAAAAGAGCAATTCCAAGCCATCAGAGG	8460
Db	8401	GTCTTACTGCAATTGAGAACTTTTGCCAGAGCAAAAGAGCAATTCCAAGCCATCAGAGG	8460
Qy	8461	GAAATTAAGCACTTCTACGTGTGTCTTAATATGTACAGATATGTACATTTTCACTTGACTTAA	8520
Db	8461	GAAATTAAGCACTTCTACGTGTGTCTTAATATGTACAGATATGTACATTTTCACTTGACTTAA	8520

Qy	8521	TACTACACACCACCT	8539
Db	8521	TACTACACACCACCT	8539

RESULT 2

ID AAD04741 standard; cDNA; 11282 BP.

AC AAD04741;

DT 17-JUL-2001 (first entry)

DE Alphaviral vector pCYTts cDNA.

KM PCV2/TS, alphavirus vector; vaccine; therapy, cancer, antiparasitic
KM antimalarial; anticancer; anti-HIV; antiviral; infectious disease;
KM Human immunodeficiency virus; HIV; influenza; passive immunisation
KM carcinoma; liver; skin; stomach; ovarian tumour; ss.

OS Rous sarcoma virus.

OS Alphavirus.
OS Unidentified.

OS chimeric.

OS chimeric.

PN WO200130989-A2.

PD 03-MAY-2001.

PF 26-OCT-2000; 2000WO-IB001557.

PR 27-OCT-1999; 99US-0161796P.

PA (CYTO-) CYTOS BIOTECHNOLOGY AG.

PA (RENN/) RENNER W A.

PA (NIEB/) NIEBA L.

PI Renner WA, Nieba L;

DR WPI; 2001-308631/32.

PT Preparing alphaviral vectors with mutations in a selected gene, for use
PT as vaccines, particularly against pathogens that mutate rapidly,
PT comprises replicating in the presence of a nucleoside analog.

PS Claim 6; Fig 3; 103pp; English.

The present invention relates to a method for preparing viral vectors which comprises inserting a gene of interest into an alphaviral vector such as PCrVts, pinteps and replicating the vector in the presence of alphaviral replicase and nucleoside analogues (5'-azacytidine (AZT), FU-5' fluorouridine) to produce a modified gene of interest. The replication is repeated until the modified gene in 90 % of the vector population contain a mutation in the modified gene which is 90-99 % identical with the gene of interest. The vector populations are used in vaccines for treatment or prevention of a wide variety of infectious diseases (viral or parasitic, e.g. human immuno deficiency virus (HIV), influenza, CC Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the mutant populations will therefore be effective against viral escape mutants. Mutagensis in a eukaryotic cell ensures that expressed proteins are correctly glycosylated. Antisera raised against the vaccines can be used for passive immunisation. The present cDNA sequence is an alphaviral vector PCrVts. The vector contains Rous Sarcoma Virus promoter, cis-acting sequence elements, non-structural proteins 1-4, gene of interest, alphavirus subgenomic promoter, ampicillin resistance marker for selection and a CoEI sequence for bacterial amplification

Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match	100.0%;	Score 8539;	DB 4;	Length 11282;
Best Local Similarity	100.0%;	Pred. No. 0;		

[illegible]

Qy	1081	GCATTTTCGATCTGGCCAGTAACTAATGAGCTGAGGTTCTTACCAAGCAGATC	1140
Db	1081	GCATTTTCGATCTGGCCAGTAACTAATGAGCTGAGGTTCTTACCAAGCAGATC	1140
Qy	1141	TTGGACATAGGACGCGACCGGCTCGTAAGATGTTTTCCAGACCAAGTATCTGTGTC	1200
Db	1141	TTGGACATAGGACGCGACCGGCTCGTAAGATGTTTTCCAGACCAAGTATCTGTGTC	1200
Qy	1201	TGCCCATGCGGTAGTCCGAAAGACCCGGACCGCATGATGAAATAGCAGTAACTGCGC	1260
Db	1201	TGCCCATGCGGTAGTCCGAAAGACCCGGACCGCATGATGAAATAGCAGTAACTGCGC	1260
Qy	1261	GAAGAACGCTGACAGATTACAAACAAGACTTGATGAGAGATTAAAGATCTCCGAGC	1320
Db	1261	GAAGAACGCTGACAGATTACAAACAAGACTTGATGAGAGATTAAAGATCTCCGAGC	1320
Qy	1321	GTAATTGATACGCGGATGCTGAAACACATCGCTCTGCTTTCAACAAGATGTTACTGC	1380
Db	1321	GTAATTGATACGCGGATGCTGAAACACATCGCTCTGCTTTCAACAAGATGTTACTGC	1380
Qy	1381	AACATGGGTGCGAATATTCGTCATGAGGACGTTATATCAACGCTCCCGGAATATC	1440
Db	1381	AACATGGGTGCGAATATTCGTCATGAGGACGTTATATCAACGCTCCCGGAATATC	1440
Qy	1441	TATCATCAGGCTATGAAAGCGTGCAGACCTCTGATGATGATGCTTCGACACCCAG	1500
Db	1441	TATCATCAGGCTATGAAAGCGTGCAGACCTCTGATGATGATGCTTCGACACCCAG	1500
Qy	1501	TTCACTGTTCTGCGCTATGCGAGGTTCCATCCCTCGTCAACACCAACTGCGGCGAG	1560
Db	1501	TTCACTGTTCTGCGCTATGCGAGGTTCCATCCCTCGTCAACACCAACTGCGGCGAG	1560
Qy	1561	AAAGTCCCTGAAGGCGCTAATCGGACTTTGAGCAACAAGCTGAGTGAAGTGAACA	1620
Db	1561	AAAGTCCCTGAAGGCGCTAATCGGACTTTGAGCAACAAGCTGAGTGAAGTGAACA	1620
Qy	1621	GGAAATTTGTCGATATGAGGAAAGAGATTGAAGCCCGGCTGCTTATTTCTCC	1680
Db	1621	GGAAATTTGTCGATATGAGGAAAGAGATTGAAGCCCGGCTGCTTATTTCTCC	1680
Qy	1681	GTAAGATGACACTTTATCCAGAACACAGACCGACTTGACAGCTGGCATCTTCATCG	1740
Db	1681	GTAAGATGACACTTTATCCAGAACACAGACCGACTTGACAGCTGGCATCTTCATCG	1740
Qy	1741	GTTGTTCCACTTGAATGGAAGCACTTGCCTGCTGTGATACAGTGTGATGCTTC	1800
Db	1741	GTTGTTCCACTTGAATGGAAGCACTTGCCTGCTGTGATACAGTGTGATGCTTC	1800
Qy	1801	GAAGGCTACGTAAGTGAAGAAATCACCATCAGTCCCGGATCAGCGGAAACCTGTGGA	1860
Db	1801	GAAGGCTACGTAAGTGAAGAAATCACCATCAGTCCCGGATCAGCGGAAACCTGTGGA	1860
Qy	1861	TACGCGGTTACACAATAGCGAGGCTTCTTGATGCAAAAGTTACTGACACAGTAAA	1920
Db	1861	TACGCGGTTACACAATAGCGAGGCTTCTTGATGCAAAAGTTACTGACACAGTAAA	1920
Qy	1921	GGAAACGGGTATGTTCCCTGTGTGACGTAATCCCGGACCATATGAGATCAAGT	1980
Db	1921	GGAAACGGGTATGTTCCCTGTGTGACGTAATCCCGGACCATATGAGATCAAGT	1980
Qy	1981	ACTGATTAATGGGACGATATATCACTGACATGCAAAAATCTTGTTGGGCTC	2040
Db	1981	ACTGATTAATGGGACGATATATCACTGACATGCAAAAATCTTGTTGGGCTC	2040
Qy	2041	AACAGGGAATTTGATTAACGATAGCTAAACAGAAACACCAACACCATGCAAAATTAAC	2100
Db	2041	AACAGGGAATTTGATTAACGATAGCTAAACAGAAACACCAACACCATGCAAAATTAAC	2100
Qy	2101	CTTCTGCCGATCATAGCAAGGGTTGAGCAATGCGGTAAAGAGCGCAAGATGATCTT	2160
Db	2101	CTTCTGCCGATCATAGCAAGGGTTGAGCAATGCGGTAAAGAGCGCAAGATGATCTT	2160
Qy	2161	GATTAACGAGAAATGCTGGGTACTAGAAACGAAAGCTTAAGTATGCTGCTGTGGCG	2220
Db	2161	GATTAACGAGAAATGCTGGGTACTAGAAACGAAAGCTTAAGTATGCTGCTGTGGCG	2220
Qy	2221	TTTGGCATTAAGAAAGTACATTCGTTTATGCCCCACTGGAACGAGACTGCGTAAA	2280
Db	2221	TTTGGCATTAAGAAAGTACATTCGTTTATGCCCCACTGGAACGAGACTGCGTAAA	2280
Qy	2281	GTCACAGCTCTTTTAAAGCTTTTCCATGTCGTCGATGAGACACTCTTGGCCATG	2340
Db	2281	GTCACAGCTCTTTTAAAGCTTTTCCATGTCGTCGATGAGACACTCTTGGCCATG	2340
Qy	2341	TGCGTAGGCAAAATTTGAAACTGACATTCGACAAACAAAGAGAGAAAACTGCTCAG	2400
Db	2341	TGCGTAGGCAAAATTTGAAACTGACATTCGACAAACAAAGAGAGAAAACTGCTCAG	2400
Qy	2401	GTCGGAAGAAATTAATGATGAGAGCCAAAGGCTCTTTTGAAGATGCTCAGAGAGAGCC	2460
Db	2401	GTCGGAAGAAATTAATGATGAGAGCCAAAGGCTCTTTTGAAGATGCTCAGAGAGAGCC	2460
Qy	2461	AGAGCGGAGAACTCCGAGAAAGCACTTCAACATTAAGTGAGCAAAAGGATCGAGCA	2520
Db	2461	AGAGCGGAGAACTCCGAGAAAGCACTTCAACATTAAGTGAGCAAAAGGATCGAGCA	2520
Qy	2521	GCGCAGAAATTTGCTGCGAAAGTGAAGGAGCTCCAGGCGGACATCGAGCAGATTAATT	2580
Db	2521	GCGCAGAAATTTGCTGCGAAAGTGAAGGAGCTCCAGGCGGACATCGAGCAGATTAATT	2580
Qy	2581	GAAGCCCCGGGTGACGTAAGTAAATCTTAAGCAAAATGACCGTATGATGAGACAG	2640
Db	2581	GAAGCCCCGGGTGACGTAAGTAAATCTTAAGCAAAATGACCGTATGATGAGACAG	2640
Qy	2641	TATATGTTGTTCTGCGCAAACTCTGTGCTGAAGAAATCCAAACTCGACCGCACCCG	2700
Db	2641	TATATGTTGTTCTGCGCAAACTCTGTGCTGAAGAAATCCAAACTCGACCGCACCCG	2700
Qy	2701	CTAGCAGATCAGGTTAAGTATTAATCACTCCGAAAGATCAGGAAGTACGCGTGA	2760
Db	2701	CTAGCAGATCAGGTTAAGTATTAATCACTCCGAAAGATCAGGAAGTACGCGTGA	2760
Qy	2761	CCATACGACGCTAAAGTATGATGTCACAGAGAGGTCCGTAATGCGCAGAAATTTCTTA	2820
Db	2761	CCATACGACGCTAAAGTATGATGTCACAGAGAGGTCCGTAATGCGCAGAAATTTCTTA	2820
Qy	2821	GCACTAGTAGAGCGCCAGTTAGTGTACAAAGAAAGAGTGTGAAACCGCAACTA	2880
Db	2821	GCACTAGTAGAGCGCCAGTTAGTGTGTACAAAGAAAGAGTGTGAAACCGCAACTA	2880
Qy	2881	TACCACTTGCATGATGACCCCGCCAGAAATACAGAAAGAGAGCAAGTTACA	2940
Db	2881	TACCACTTGCATGATGACCCCGCCAGAAATACAGAAAGAGAGCAAGTTACA	2940
Qy	2941	AAGGCAAGCTTGCAAAACAGATACGTGTTGAAGCTGGAACAAAGCGTTGGTTAAG	3000
Db	2941	AAGGCAAGCTTGCAAAACAGATACGTGTTGAAGCTGGAACAAAGCGTTGGTTAAG	3000
Qy	3001	AAGGAAAGCTCAGGTCTGTCCTCTCGGAGAAATGACCAACCTCCCTATCATGAG	3060
Db	3001	AAGGAAAGCTCAGGTCTGTCCTCTCGGAGAAATGACCAACCTCCCTATCATGAG	3060
Qy	3061	CTAGCTCTGAGGAGCTGGAAGACCCGACCTGCGGTCCCGTACAAAGTCAAAATAGGA	3120
Db	3061	CTAGCTCTGAGGAGCTGGAAGACCCGACCTGCGGTCCCGTACAAAGTCAAAATAGGA	3120
Qy	3121	GTGATAGGACACCGGGGTGCGGCAATTAATTAAGTCAACTGTCAACGCGACA	3180
Db	3121	GTGATAGGACACCGGGGTGCGGCAATTAATTAAGTCAACTGTCAACGCGACA	3180
Qy	3181	GATCTGTTTACAGCGGGAAGAAAGAAATTTGCGGAAATTTGAAGGCGCAGTGTAGA	3240
Db	3181	GATCTGTTTACAGCGGGAAGAAAGAAATTTGCGGAAATTTGAAGGCGCAGTGTAGA	3240
Qy	3241	CTGAGGGGTATGACAGATTAGCTGAAAGACAGTAGATTGCGTTATGCTCAACGATGCGAC	3300

Db 3241 CTGAGGGGATGACGATTACCTGACAGACAGTACGATTGCTTACGATGCGAC 3300
QY 3301 AAAGCCGAGAAAGTGTGATGAGTGAAGAGCGTTGCGTGCACAGAGAGCACTT 3360
Db 3301 AAAGCCGAGAAAGTGTGATGAGTGAAGAGCGTTGCGTGCACAGAGAGCACTT 3360
QY 3361 GCCTGATTTGCTATCGTACAGGCCCCGCAAGAGTACTATGCGAGAGCCCATCAA 3420
Db 3361 GCCTGATTTGCTATCGTACAGGCCCCGCAAGAGTACTATGCGAGAGCCCATCAA 3420
QY 3421 TGCGGATTTCTTCAACATGATGCACTAAAGTACATTCACTGCCTGAAAAAGACATA 3480
Db 3421 TGCGGATTTCTTCAACATGATGCACTAAAGTACATTCACTGCCTGAAAAAGACATA 3480
QY 3481 TGACACAGACATCTCAAGATATATCTCCGCGGTTGACACAGCCAGTTACGCTATT 3540
Db 3481 TGACACAGACATCTCAAGATATATCTCCGCGGTTGACACAGCCAGTTACGCTATT 3540
QY 3541 GTATCGACACTGATTAAGATGAGAAAGTGAACCAAGAACCCGTGCAAGAGACATT 3600
Db 3541 GTATCGACACTGATTAAGATGAGAAAGTGAACCAAGAACCCGTGCAAGAGACATT 3600
QY 3601 GAAATCGATATTAAGAGGGGCCAAGAGCCGAGGCGATATCATCTTGAATGTTTC 3660
Db 3601 GAAATCGATATTAAGAGGGGCCAAGAGCCGAGGCGATATCATCTTGAATGTTTC 3660
QY 3661 CGCGGGTGGGTTAAGCAATTGCAATGCACTATCCCGGACATGAAGTATGACGCGCG 3720
Db 3661 CGCGGGTGGGTTAAGCAATTGCAATGCACTATCCCGGACATGAAGTATGACGCGCG 3720
QY 3721 GCTTCACAGAGGCTTAACAGAAAGAGTGTATGCGTCCGGCAAAAAGTCAATGAAC 3780
Db 3721 GCTTCACAGAGGCTTAACAGAAAGAGTGTATGCGTCCGGCAAAAAGTCAATGAAC 3780
QY 3781 CCACTGACGCGATCAGATGAGACATGTAAGTGTGCTGACCCGCACTGAGAGACAG 3840
Db 3781 CCACTGACGCGATCAGATGAGACATGTAAGTGTGCTGACCCGCACTGAGAGACAG 3840
QY 3841 CTAGTGTGAAAACTTTCAGAGGCGGACCCATGATTAAGAGCCCACTAACATCTTAA 3900
Db 3841 CTAGTGTGAAAACTTTCAGAGGCGGACCCATGATTAAGAGCCCACTAACATCTTAA 3900
QY 3901 GGAACCTTTTCAAGGCTTATAGAGACTGAGAGCTGAAACAAGAGAAATTAATGTCGA 3960
Db 3901 GGAACCTTTTCAAGGCTTATAGAGACTGAGAGCTGAAACAAGAGAAATTAATGTCGA 3960
QY 3961 ATAAACAGCCCACTCCCGGCGCAATCCGTTCACTGCAAGAGCAACGTTTCTGGCG 4020
Db 3961 ATAAACAGCCCACTCCCGGCGCAATCCGTTCACTGCAAGAGCAACGTTTCTGGCG 4020
QY 4021 AAAGCATTTGAAACGATATAGCAAGCGGCGGATCTTACCTTACCGTTGCCAGTGAAG 4080
Db 4021 AAAGCATTTGAAACGATATAGCAAGCGGCGGATCTTACCTTACCGTTGCCAGTGAAG 4080
QY 4081 GAACTGTTCCTCAAGTTCGAGATGACAAACACATTCGCGCAATTAACGCTTAGACGTA 4140
Db 4081 GAACTGTTCCTCAAGTTCGAGATGACAAACACATTCGCGCAATTAACGCTTAGACGTA 4140
QY 4141 ATTTGATTAAGTTTTCGCGATGGAATTGACAAAGGAGCTGTTTCTAAGAGAGATC 4200
Db 4141 ATTTGATTAAGTTTTCGCGATGGAATTGACAAAGGAGCTGTTTCTAAGAGAGATC 4200
QY 4201 CCACTAACGTAACATCCCGCGATTCAGCGAGGCGGATGCTTATGGAACAAGCCCA 4260
Db 4201 CCACTAACGTAACATCCCGCGATTCAGCGAGGCGGATGCTTATGGAACAAGCCCA 4260
QY 4261 GGAACCCGCAAGTATGAGTACGATCAGCGCAATTCGCGCACTTCCCTAATTTCCG 4320
Db 4261 GGAACCCGCAAGTATGAGTACGATCAGCGCAATTCGCGCACTTCCCTAATTTCCG 4320
QY 4321 GTGTTCAAGTAGTGGGAGGCGACCACTTGAATTTGCAAGCGGAGAGAACAGATT 4380

Db 4321 GTGTTCAAGTAGTGGGAGGCGACCACTTGAATTTGCAAGCGGAGAGAACAGATT 4380
QY 4381 ATCTTGACAGATTAACCTGTCGCGGAGAACCGGAATCTTCTCAAGCTTAATGTC 4440
Db 4381 ATCTTGACAGATTAACCTGTCGCGGAGAACCGGAATCTTCTCAAGCTTAATGTC 4440
QY 4441 GAGTACAGAGAGCAACCCGCGCGTCAAAAAATTTCTTGAACAGTTCAAAACACAC 4500
Db 4441 GAGTACAGAGAGCAACCCGCGCGTCAAAAAATTTCTTGAACAGTTCAAAACACAC 4500
QY 4501 TCAGTACTTGTGATCAAGAGAAAAATTTGAAGCTCCCGTGAAGAAATCGAATGATC 4560
Db 4501 TCAGTACTTGTGATCAAGAGAAAAATTTGAAGCTCCCGTGAAGAAATCGAATGATC 4560
QY 4561 GCGCCGATTTGGCATACCGGATGAGTAAAGTAACTAACCTGGCTTTCGGGTTTCGCGG 4620
Db 4561 GCGCCGATTTGGCATACCGGATGAGTAAAGTAACTAACCTGGCTTTCGGGTTTCGCGG 4620
QY 4621 CAGGCAAGGTAAGCACTGTGTTCAATCAATTTGAACTAAATACAGAAACCACTTT 4680
Db 4621 CAGGCAAGGTAAGCACTGTGTTCAATCAATTTGAACTAAATACAGAAACCACTTT 4680
QY 4681 CAGCAATGCAAGACCATGCGGACCTTAAACCTTTTCGCTTCCGCTGAAATGAT 4740
Db 4681 CAGCAATGCAAGACCATGCGGACCTTAAACCTTTTCGCTTCCGCTGAAATGAT 4740
QY 4741 TTAATCTCAGAGAGCACTCGTGTGAGTCTTATGCTAGCGGACCGCAACAGTGA 4800
Db 4741 TTAATCTCAGAGAGCACTCGTGTGAGTCTTATGCTAGCGGACCGCAACAGTGA 4800
QY 4801 GACGTAGTACCGCTTTGCCAGAAAGTTTGTCAAGGTTCTGACAGAGACAGATTGT 4860
Db 4801 GACGTAGTACCGCTTTGCCAGAAAGTTTGTCAAGGTTCTGACAGAGACAGATTGT 4860
QY 4861 GTCTCAAGAAATACAGAAATGTAACCTGATTTCCGACCACTAGCAACAGCCGTACAGG 4920
Db 4861 GTCTCAAGAAATACAGAAATGTAACCTGATTTCCGACCACTAGCAACAGCCGTACAGG 4920
QY 4921 CAATTACCCCGCACCATGTAATGCGGATTTGCGTCCGTATGAGGAGTACAGAGAT 4980
Db 4921 CAATTACCCCGCACCATGTAATGCGGATTTGCGTCCGTATGAGGAGTACAGAGAT 4980
QY 4981 GGAATTGAGCCGCGCTCATACCGCACCAAAAGGAGATATGCTGATCAAGAG 5040
Db 4981 GGAATTGAGCCGCGCTCATACCGCACCAAAAGGAGATATGCTGATCAAGAG 5040
QY 5041 GAAAGCTTTGAAAGCGAGCCCAATCCGCTGCTTAAACAGAGGAGATCTGCGTGC 5100
Db 5041 GAAAGCTTTGAAAGCGAGCCCAATCCGCTGCTTAAACAGAGGAGATCTGCGTGC 5100
QY 5101 ATCTATTAACGTTGGCGGACAGTTTACCGATTGACGACAGGAGACAGCCAGAGA 5160
Db 5101 ATCTATTAACGTTGGCGGACAGTTTACCGATTGACGACAGGAGACAGCCAGAGA 5160
QY 5161 ATGACTGTGTGCTTGAAGAAAGATGATCAAGCGGCTGCGCTGATTTCCGGAAGCAC 5220
Db 5161 ATGACTGTGTGCTTGAAGAAAGATGATCAAGCGGCTGCGCTGATTTCCGGAAGCAC 5220
QY 5221 CCAGAAAGCAAGCCCTGAAATTTGCTAACAAAGCGCTACAGAGCTGCGACACTTAGTA 5280
Db 5221 CCAGAAAGCAAGCCCTGAAATTTGCTAACAAAGCGCTACAGAGCTGCGACACTTAGTA 5280
QY 5281 AATGAACATTAACATCAAGTGTGCGCATTCATGCTTATCTACAGGCAATTAACGAGCC 5340
Db 5281 AATGAACATTAACATCAAGTGTGCGCATTCATGCTTATCTACAGGCAATTAACGAGCC 5340
QY 5341 GGAAGAAAGCCGCTTGAAGTATCACTTAACTGCTTGAACAACGCGCTAGACAGAACTGAC 5400
Db 5341 GGAAGAAAGCCGCTTGAAGTATCACTTAACTGCTTGAACAACGCGCTAGACAGAACTGAC 5400
QY 5401 GCGGACGTAAACATTAATGCTGATTAAGAGTGAAGAGAAAGAAATGACAGCGGCACTC 5460
Db 5401 GCGGACGTAAACATTAATGCTGATTAAGAGTGAAGAGAAAGAAATGACAGCGGCACTC 5460

QY	5461	CAACTTAAAGAGCTCTGTAAACAGACTGAAGGATGAAGTATAGAGATCGACGAGACTTAA	5520
Db	5461	CAACTTAAAGAGCTCTGTAAACAGACTGAAGGATGAAGTATAGAGATCGAGAGACTTAA	5520
QY	5521	GTATGGAATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTACAAAGGA	5580
Db	5521	GTATGGAATTCATCCAGACAGTTGCTTGAAGGGAAGAAAGGATTCAGTACTACAAAGGA	5580
QY	5581	AAATTTGATTTGTACTTCTGAAAGGCCAAATTCCATCAAGCAGCAAAAGCATGGCCGAG	5640
Db	5581	AAATTTGATTTGTACTTCTGAAAGGCCAAATTCCATCAAGCAGCAAAAGCATGGCCGAG	5640
QY	5641	ATTAAGGCTCTGTTCCCTTAATGACAGAGAAAGTATGAACAATGTGGCTTACATATTG	5700
Db	5641	ATTAAGGCTCTGTTCCCTTAATGACAGAGAAAGTATGAACAATGTGGCTTACATATTG	5700
QY	5701	GGTAGAGCAATGAGAAACAATCCGCGAAAAGTGCCCGGTGACATTAACCCGTGCTTAGC	5760
Db	5701	GGTAGAGCAATGAGAAACAATCCGCGAAAAGTGCCCGGTGACATTAACCCGTGCTTAGC	5760
QY	5761	CCGCCCAAAAGGTTGCGCGTCTTGTGATGATGTCAGTAAGCAGCAAGAAAGGCTCACAGA	5820
Db	5761	CCGCCCAAAAGGTTGCGCGTCTTGTGATGATGTCAGTAAGCAGCAAGAAAGGCTCACAGA	5820
QY	5821	CTTAGAAGCAATTAACGTCAAGAAAGATTACATATGCTCTCCACCCCTTCTTAACAC	5880
Db	5821	CTTAGAAGCAATTAACGTCAAGAAAGATTACATATGCTCTCCACCCCTTCTTAACAC	5880
QY	5881	AAAAATTAAGATGTTCAGAGAGTTCAGTGACAGAAAGTATGTCCTGTTTAATCCGACACT	5940
Db	5881	AAAAATTAAGATGTTCAGAGAGTTCAGTGACAGAAAGTATGTCCTGTTTAATCCGACACT	5940
QY	5941	CCCGCATTCGTTCCCGCCCGTAAAGTACATTAAGAGCCAGAAACAGCTACCGCTCTCCT	6000
Db	5941	CCCGCATTCGTTCCCGCCCGTAAAGTACATTAAGAGCCAGAAACAGCTACCGCTCTCCT	6000
QY	6001	GCACAGGCCGAGAGAGGCCCCCGAAATTGTAGCGACACCGTCACCATCTTACAGCTATTAAC	6060
Db	6001	GCACAGGCCGAGAGAGGCCCCCGAAATTGTAGCGACACCGTCACCATCTTACAGCTATTAAC	6060
QY	6061	ACCTCCGCTTGAATGTACAGACATCTCACTGGATATGATGACATTAAGCGAAGGCTCACTT	6120
Db	6061	ACCTCCGCTTGAATGTACAGACATCTCACTGGATATGATGACATTAAGCGAAGGCTCACTT	6120
QY	6121	TTTTTCGAGCTTTTAAAGCGAGTCCGACAACTCTATTACTAGTATAGCAAGTGGTCTCTACGA	6180
Db	6121	TTTTTCGAGCTTTTAAAGCGAGTCCGACAACTCTATTACTAGTATAGCAAGTGGTCTCTACGA	6180
QY	6181	CTTAGATTCACTAGAGATATAGTACCCGAAAGGACGAGTGTGGTGGCTGACGTTCAATGCCGT	6240
Db	6181	CTTAGATTCACTAGAGATATAGTACCCGAAAGGACGAGTGTGGTGGCTGACGTTCAATGCCGT	6240
QY	6241	CAAGAGCCCTGCCCCCTTAATCCACCGCAAGGCTTAAGAAAGATGGCCCGCTGGCAGCGGCA	6300
Db	6241	CAAGAGCCCTGCCCCCTTAATCCACCGCAAGGCTTAAGAAAGATGGCCCGCTGGCAGCGGCA	6300
QY	6301	AGAAAAGAGCCCACTCCAACGCGCAAGCAATAGCTCTGAGTCCCTCAACTCTCTTTTGGT	6360
Db	6301	AGAAAAGAGCCCACTCCAACGCGCAAGCAATAGCTCTGAGTCCCTCAACTCTCTTTTGGT	6360
QY	6361	GGGGTATTCATATGTCCCTCGGATCAATTTTTCAGCGAGAGACGGCCCGCAAGCAGCGGTA	6420
Db	6361	GGGGTATTCATATGTCCCTCGGATCAATTTTTCAGCGAGAGACGGCCCGCAAGCAGCGGTA	6420
QY	6421	CAACCCCTGGCAACAGGCCCAAGCGATGTGCTTATGTTTCGAGTCTTTTCCGACGGA	6480
Db	6421	CAACCCCTGGCAACAGGCCCAAGCGATGTGCTTATGTTTCGAGTCTTTTCCGACGGA	6480
QY	6481	GAGATTGATGAGCTGAGCCGCAAGATACTAGTCCGAACCCGTCCTGTTGGATCATTT	6540
Db	6481	GAGATTGATGAGCTGAGCCGCAAGATACTAGTCCGAACCCGTCCTGTTGGATCATTT	6540

QY	6541	GAACCGGGCGCAACTGAACTCAATTATATATGTCGCGATCAAGCCGTATCTTTTCACACTACG	6600
Db	6541	GAACCGGGCGCAAGTGAATCTCAATTATATGTCGCCGATACGCCGTATCTTTTCACACTACG	6600
QY	6601	AAGCAGAGAGGTGAGACGACGAGACGAGAGACTGAATCTGACTTAACCGGGGTAGTGGG	6660
Db	6601	AAGCAGAGAGGTGAGACGACGAGACGAGAGAGACTGAATCTGACTTAACCGGGGTAGTGGG	6660
QY	6661	TACATATTTTTCGACGGAACAGGCGCTTGGGCACTTTCGCAAAAGAAAGTCCGTTCTGCAGAAC	6720
Db	6661	TACATATTTTTCGACGGAACAGGCGCTTGGGCACTTTCGCAAAAGAAAGTCCGTTCTGCAGAAC	6720
QY	6721	CAGCTTACAAACCCGACTTTGAGAGCCCAATGTCTCTGGAAAAGAAATTCACTCCCGGTGCTC	6780
Db	6721	CAGCTTACAAACCCGACTTTGAGAGCCCAATGTCTCTGGAAAAGAAATTCACTCCCGGTGCTC	6780
QY	6781	GACACGTCTGAAAGNGAACAACCTCAAACTCAGGTATCAGATGATGCCACGAACTCAAC	6840
Db	6781	GACACGTCTGAAAGNGAACAACCTCAAACTCAGGTATCAGATGATGCCACGAACTCAAC	6840
QY	6841	AAAAGTAGTAGCAGATCTCGTAAAGTAGAAAAATCAGAAAAGCCATTAACACTGAGGCACTA	6900
Db	6841	AAAAGTAGTAGCAGATCTCGTAAAGTAGAAAAATCAGAAAAGCCATTAACACTGAGGCACTA	6900
QY	6901	CTGTCAAGACTACGACTGTATTAACCTCTGCCACAGATCAAGCCGAATTCGTATTAAGTCAAC	6960
Db	6901	CTGTCAAGACTACGACTGTATTAACCTCTGCCACAGATCAAGCCGAATTCGTATTAAGTCAAC	6960
QY	6961	TATCCGAAACCATTTGTATCTCCATAGACGTACCGGGCAACTACTCCGATCTCACAGTTCCGT	7020
Db	6961	TATCCGAAACCATTTGTATCTCCATAGACGTACCGGGCAACTACTCCGATCTCACAGTTCCGT	7020
QY	7021	GTAGCTGTCTGTAAACAATCTCTGCATGAGAACTATCCGACAGTAGACATCTTATCAGATT	7080
Db	7021	GTAGCTGTCTGTAAACAATCTCTGCATGAGAACTATCCGACAGTAGACATCTTATCAGATT	7080
QY	7081	ACTGACGAGTAGACGATGCTTACTTGATATGTATGACGAGACAGTGCATGCTCGATACT	7140
Db	7081	ACTGACGAGTAGACGATGCTTACTTGATATGTATGACGAGACAGTGCATGCTCGATACT	7140
QY	7141	GCAACCTTCTGCCCCGCTAAGCTTAAGTATCCGAAAAACATGAGATATGAGACCCCG	7200
Db	7141	GCAACCTTCTGCCCCGCTAAGCTTAAGTATCCGAAAAACATGAGATATGAGACCCCG	7200
QY	7201	AATATCCGCAAGTCGGTTCATCAGGATGACGAAACACGCTCAAAATGTGCTCATTTGCC	7260
Db	7201	AATATCCGCAAGTCGGTTCATCAGGATGACGAAACACGCTCAAAATGTGCTCATTTGCC	7260
QY	7261	GCAACTTAAAGAAATTCGACGATCAGCGACGATGCGTGAATCTGCCAACACTGAGCTCAGCG	7320
Db	7261	GCAACTTAAAGAAATTCGACGATCAGCGACGATGCGTGAATCTGCCAACACTGAGCTCAGCG	7320
QY	7321	ACATTCGAATGTCGAATGCTTTGCAAAATATGCAATGATATGACGAGTATTTGGAGAGATTC	7380
Db	7321	ACATTCGAATGTCGAATGCTTTGCAAAATATGCAATGATATGACGAGTATTTGGAGAGATTC	7380
QY	7381	GCTCGGAAAGCCAAATTAGAGTATACCACTGAGTTTGTACCCGCAATATGTAGCTTAGCTGAAA	7440
Db	7381	GCTCGGAAAGCCAAATTAGAGTATACCACTGAGTTTGTACCCGCAATATGTAGCTTAGCTGAAA	7440
QY	7441	GGCCCTTAAGGCGCGCGCACTATTTCGMAAGACGTATATTTTGGTCCCATTTGCAGAAAGTG	7500
Db	7441	GGCCCTTAAGGCGCGCGCGCACTATTTCGMAAGACGTATATTTTGGTCCCATTTGCAGAAAGTG	7500
QY	7501	CCTATGATATGATTTCTGTCATGGAACATGAAAAGAGAGCTGAAAAGTTTACACACGAGCCGAAA	7560
Db	7501	CCTATGATATGATTTCTGTCATGGAACATGAAAAGAGAGCTGAAAAGTTTACACACGAGCCGAAA	7560
QY	7561	CACACAGAAAGAAAGACGAAAGTAGCAAGTAGTACAAGCGCGCAAGACCCCTGGCGACTGCT	7620
Db	7561	CACACAGAAAGAAAGACGAAAGTAGCAAGTAGTACAAGCGCGCAAGACCCCTGGCGACTGCT	7620
QY	7621	TACTTATGCGGAGATTCAACGGGAAATTATGTGCGTAGGCTTACGCGCGCTTGTGCTTCAAC	7680

QY	30	GTGACGCTTGTTGCTCAACCTGGAACAAACATCGAACCCCATCTGGTCTAATCTTTGATT	360
Db	301	GTGACGCTTGTTGCTCAACCTGGAACAAACATCGAACCCCATCTGGTCTAATCTTTGATT	360
QY	361	TATAAGGAGATTTCGCCGATTTTCGGCTATAGTTGTTAAAAATGAGCTGATTTAACAAAT	420
Db	361	TATAAGGAGATTTCGCCGATTTTCGGCTATAGTTGTTAAAAATGAGCTGATTTAACAAAT	420
QY	421	TTAAACGGGAATTTTAAACAAATATTAAACGCTTACAAATTTCCATTCCGCTTACAGGCTGCG	480
Db	421	TTAAACGGGAATTTTAAACAAATATTAAACGCTTACAAATTTCCATTCCGCTTACAGGCTGCG	480
QY	481	CAACTGTGTGGGAAGGGGGATCGGTGGGGGGCCCTTCGCTATTATGAGCGAGCTGGGAAGG	540
Db	481	CAACTGTGTGGGAAGGGGGATCGGTGGGGGGCCCTTCGCTATTATGAGCGAGCTGGGAAGG	540
QY	541	GGGATGTGCTGTCAGAGCGCATTTAAGTTGGGTAAACCCAGGGTTTCCAGTCCAGACGTTG	600
Db	541	GGGATGTGCTGTCAGAGCGCATTTAAGTTGGGTAAACCCAGGGTTTCCAGTCCAGACGTTG	600
QY	601	TAAAAACGACGGCCAGTGAAGCGCGCAATTAACCTCTCATAAAGGAAACAAAGCTGGCTAG	660
Db	601	TAAAAACGACGGCCAGTGAAGCGCGCAATTAACCTCTCATAAAGGAAACAAAGCTGGCTAG	660
QY	661	TGGATCCAGTCTTATGCAATACCTCTTGAGTCTTGCAACATGGTAAAGATGATTAACAA	720
Db	661	TGGATCCAGTCTTATGCAATACCTCTTGAGTCTTGCAACATGGTAAAGATGATTAACAA	720
QY	721	CATGCGCTTACAAAGAGAGAAAAAGCAACCGTGCATGCGCATTTGGTGGAAAGTAAAGTGGTAC	780
Db	721	CATGCGCTTACAAAGAGAGAAAAAGCAACCGTGCATGCGCATTTGGTGGAAAGTAAAGTGGTAC	780
QY	781	GATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGTGACATGAGATTGAGCAACCACTGAA	840
Db	781	GATCGTGCCTTATTAGGAAGGCAACAGACGGGCTGTGACATGAGATTGAGCAACCACTGAA	840
QY	841	TTCCGCGATTGAGAGATTTGTGATTTAAGTCCCTCACTCGATACCGTCCGAGATTGACGG	900
Db	841	TTCCGCGATTGAGAGATTTGTGATTTAAGTCCCTCACTCGATACCGTCCGAGATTGACGG	900
QY	901	CGTAGTACACACTATTGAATCAAAACAGCGCAACAAATTCACCTACCATACAAATGGAAG	960
Db	901	CGTAGTACACACTATTGAATCAAAACAGCGCAACAAATTCACCTACCATACAAATGGAAG	960
QY	961	CCAGTAGTAAACGTAGACGTAGACCCCGAGAGTCCGTTGTCTGTGCAACTGCAAAAAAGC	1020
Db	961	CCAGTAGTAAACGTAGACGTAGACCCCGAGAGTCCGTTGTCTGTGCAACTGCAAAAAAGC	1020
QY	1021	TTCCCGCAATTTGAGGTAGTACACAGAGGTCACTCCAAATGACATGCTAAATGCGCAGA	1080
Db	1021	TTCCCGCAATTTGAGGTAGTACACAGAGGTCACTCCAAATGACATGCTAAATGCGCAGA	1080
QY	1081	GCAATTTTGGCACTGCGCCAGTAACTAATCGAGCTGGAGGTTCTTACCAACAGCGACGATC	1140
Db	1081	GCAATTTTGGCACTGCGCCAGTAACTAATCGAGCTGGAGGTTCTTACCAACAGCGACGATC	1140
QY	1141	TTGGAACATAGGCAAGCGACACCGGCTCGTAGAATGTTTTCCGAGACACATATCATTTGTGTC	1200
Db	1141	TTGGAACATAGGCAAGCGACACCGGCTCGTAGAATGTTTTCCGAGACACATATCATTTGTGTC	1200
QY	1201	TGCCCCATGCGTAGTCCAGAAAGACCCCGAGCCGATGATGAATACCGAGTAAACTGGCG	1260
Db	1201	TGCCCCATGCGTAGTCCAGAAAGACCCCGAGCCGATGATGAATACCGAGTAAACTGGCG	1260
QY	1261	GAAAAAGGTGCAAAATTTAAACAAAGAACTTGGCATGGAAGATTAAAGATCTCCGAGAC	1320
Db	1261	GAAAAAGGTGCAAAATTTAAACAAAGAACTTGGCATGGAAGATTAAAGATCTCCGAGAC	1320
QY	1321	GTACTTGAATACGCGCGAGTGTGAAACACCATGCTCTCTTTCAACAGATTTAATCTGAC	1380
Db	1321	GTACTTGAATACGCGCGAGTGTGAAACACCATGCTCTCTCTTTCAACAGATTTAATCTGAC	1380
QY	1381	AACATGCGTCCCGAATATTTCCGTACTGACAGACGTGTATATCAACGCTCCCGGAATATC	1440

Db	1381	AAATGCGTCCGGAATATTCCTGTCATGACAGACGTGATATATCAACGCTCCCGGAATATAC	1440
Qy	1441	TATCATGAGCTATGAAAAGCGTGCAGACCCCTGTACTGTGATTTGGCTTGACACCAACCCAG	1500
Db	1441	TATCATGAGCTATGAAAAGCGTGCAGACCCCTGTACTGTGATTTGGCTTGACACCAACCCAG	1500
Qy	1501	TTCAATGTTCTCCGGTATAGGAGAGGTTGCTACCCCTGCGTACAACAACCAACTGGGGCCGAGAG	1560
Db	1501	TTCAATGTTCTCCGGTATAGGAGAGGTTGCTACCCCTGCGTACAACAACCAACTGGGGCCGAGAG	1560
Qy	1561	AAAGTCCCTTAAGCGCGTAAACATCGACTTTTGACGACAAAGCTGAGTGAAGTAGAGACA	1620
Db	1561	AAATCTCTTGAAGCGCTTAACATCGACTTTTGACGACAAAGCTGAGTGAAGTAGAGACA	1620
Qy	1621	GGAAAATTGTCGATATAGGAGAGAGAGTTGAAGCCCGGGGTGCGGCTTATTTTCTCC	1680
Db	1621	GGAAAATTGTCGATATAGGAGAGAGAGTTGAAGCCCGGGGTGCGGCTTATTTTCTCC	1680
Qy	1681	GTAGAGTCGACACTTTTATCCAGAACAGAGCCAGCTTGACAGACTGGCACTTTCATCG	1740
Db	1681	GTAGAGTCGACACTTTTATCCAGAACAGAGCCAGCTTGACAGACTGGCACTTTCATCG	1740
Qy	1741	GTTGTTCCACTTGAATGGAAGACAGTCTGTACACTTCCGCTGTGTATACAGTGGTAGTTGC	1800
Db	1741	GTTGTTCCACTTGAATGGAAGACAGTCTGTACACTTCCGCTGTGTATACAGTGGTAGTTGC	1800
Qy	1801	GAAAGCTACGTAGTGAAGAAAATACCAATCAGTCCGCGGATCAGCGGAGAAAACCGTGGGA	1860
Db	1801	GAAAGCTACGTAGTGAAGAAAATACCAATCAGTCCGCGGATCAGCGGAGAAAACCGTGGGA	1860
Qy	1861	TACCGCGTTACACACATAGCGAGGGCTTCTTGCTATAGCAAAAGTTATCTGCACACGTATAA	1920
Db	1861	TACCGCGTTACACACATAGCGAGGGCTTCTTGCTATAGCAAAAGTTATCTGCACACGTATAA	1920
Qy	1921	GGAGAACGGGATGCTGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG	1980
Db	1921	GGAGAACGGGATGCTGTTCCCTGTGTGCACGTACATCCCGGCCACCATATGCGATCAGATG	1980
Qy	1981	ACTGCTATTAATGACCACGAGTATATCACTGACAGATGACAAAACTTTCTGTTGGGCTC	2040
Db	1981	ACTGCTATTAATGACCACGAGTATATCACTGACAGATGACAAAACTTTCTGTTGGGCTC	2040
Qy	2041	AACCAAGGAATTTGCTATTACGGTAGACTATACACGAAACACCAACCATATGCAAAATTAC	2100
Db	2041	AACCAAGGAATTTGCTATTACGGTAGACTATACACGAAACACCAACCATATGCAAAATTAC	2100
Qy	2101	CTTCTGCCGATCATAGCACAAGGGTTACGAAATAGGGCTAAGAGCGCAAGATGATCTT	2160
Db	2101	CTTCTGCCGATCATAGCACAAGGGTTACGAAATAGGGCTAAGAGCGCAAGATGATCTT	2160
Qy	2161	GATAACGGAATAATGCTGGGTACTAGAGAACGCAAGCTTTACGTATGGCTGTGTGGGCG	2220
Db	2161	GATAACGGAATAATGCTGGGTACTAGAGAACGCAAGCTTTACGTATGGCTGTGTGGGCG	2220
Qy	2221	TTTTCGCACTAAGAAAGTACATTCCTTTATATGCCCACTCGAAGCGCAGACCTCGGTATAA	2280
Db	2221	TTTTCGCACTAAGAAAGTACATTCCTTTATATGCCCACTCGAAGCGCAGACCTCGGTATAA	2280
Qy	2281	GTCCAGCTCTTTTAAGCGCTTTTCCCATATGTCGTCGATAGAGAGACCTCTTTGGCCATG	2340
Db	2281	GTCCAGCTCTTTTAAGCGCTTTTCCCATATGTCGTCGATAGAGAGACCTCTTTGGCCATG	2340
Qy	2341	TCGCTGAGGCGAATAATGAAATCGGCAATTGCAACCAAGAGAGAGAAAATCTGCTCAG	2400
Db	2341	TCGCTGAGGCGAATAATGAAATCGGCAATTGCAACCAAGAGAGAGAAAATCTGCTCAG	2400
Qy	2401	GTTCTCGAGGAATTAATGTCATGAGAGCGCAAGGCTGCTTTTGAAGATGCTCAGAGAGAACCC	2460
Db	2401	GTTCTCGAGGAATTAATGTCATGAGAGCGCAAGGCTGCTTTTGAAGATGCTCAGAGAGAACCC	2460
Qy	2461	AGAGCGGAGAGCTCCGAGAGGCACTTCCACATTAATGAGGAGACAAAGGATGAGGCA	2520
Db	2461	AGAGCGGAGAGCTCCGAGAGGCACTTCCACATTAATGAGGAGACAAAGGATGAGGCA	2520

D 2461 AGACGGAGAGACTCCGAGAAAGCATTCACACATTAGTGCAGACAAAGGCATCGAGGCA 2520
Q 2521 GCCGCAAGATTGCTGCGAAGTGAAGGGCTCCAGCGGACATCGAGAGCATTAATT 2580
D 2521 GCCGCAAGATTGCTGCGAAGTGAAGGGCTCCAGCGGACATCGAGAGCATTAATT 2580
Q 2581 GAAACCCCGCGGTCACTGAAGATTAATCTCAAGCAAAATGACCGTATGATCGACAG 2640
D 2581 GAAACCCCGCGGTCACTGAAGATTAATCTCAAGCAAAATGACCGTATGATCGACAG 2640
Q 2641 TATATGTTGTCGCGCAAACTGTCGTGAAGATGCAAACTCGGACACGAGGCAACCG 2700
D 2641 TATATGTTGTCGCGCAAACTGTCGTGAAGATGCAAACTCGGACACGAGGCAACCG 2700
Q 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCGGAGATCAGAAAGTACGCGGTGAA 2760
D 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCGGAGATCAGAAAGTACGCGGTGAA 2760
Q 2761 CCATACGACCTTAAAGTACTGATGCGCAGCAGAGGTGCGGTACCATGCGCAAACTCTA 2820
D 2761 CCATACGACCTTAAAGTACTGATGCGCAGCAGAGGTGCGGTACCATGCGCAAACTCTA 2820
Q 2821 GCACTGAGTAGAGCCGACGTTAAGTATCAAGAAAGAGATTGTGAACCGAACTA 2880
D 2821 GCACTGAGTAGAGCCGACGTTAAGTATCAAGAAAGAGATTGTGAACCGAACTA 2880
Q 2881 TACCACATTCGATGCAATGAGCCCGCCAGAAATACAGAAAGAGCAGTACAAAGTTACA 2940
D 2881 TACCACATTCGATGCAATGAGCCCGCCAGAAATACAGAAAGAGCAGTACAAAGTTACA 2940
Q 2941 AAGCAGAGCTTGCAGAAACAGAGTACGTGTTGACGTGACAAAGAGCTTGCCTTAAG 3000
D 2941 AAGCAGAGCTTGCAGAAACAGAGTACGTGTTGACGTGACAAAGAGCTTGCCTTAAG 3000
Q 3001 AAGGAAAGACCTCAGGTCGTGCTCTCGGAGAACTGACCAACCTCCCTATCATAG 3060
D 3001 AAGGAAAGACCTCAGGTCGTGCTCTCGGAGAACTGACCAACCTCCCTATCATAG 3060
Q 3061 CTAGCTCTGAGGAGCTGAAGACCCGACCTGCGGTCCGTTACAAAGTCGAAACATAGGA 3120
D 3061 CTAGCTCTGAGGAGCTGAAGACCCGACCTGCGGTCCGTTACAAAGTCGAAACATAGGA 3120
Q 3121 GTGATAGGCAACCGGGGTGGGCAATGACTTATCAAGTCACTGTCAACGCGACGA 3180
D 3121 GTGATAGGCAACCGGGGTGGGCAATGACTTATCAAGTCACTGTCAACGCGACGA 3180
Q 3181 GATCTTGTACACGCGGAAAGAAATTTGCGCAAAATGAGGCGCAGTGTAGA 3240
D 3181 GATCTTGTACACGCGGAAAGAAATTTGCGCAAAATGAGGCGCAGTGTAGA 3240
Q 3241 CTGAGGGGATGAGATTAAGTGAAGACAGTACGATTGCTCAACGATGCGAC 3300
D 3241 CTGAGGGGATGAGATTAAGTGAAGACAGTACGATTGCTCAACGATGCGAC 3300
Q 3301 AAAGCGGTAGAAGTGTGTCGTTGACGAAGCGTTGCGGTGCGACGAGAGCACTAATT 3360
D 3301 AAAGCGGTAGAAGTGTGTCGTTGACGAAGCGTTGCGGTGCGACGAGAGCACTAATT 3360
Q 3361 GCGTTGTTGCTATCGTCAGAGCCCGCAAGAGGTAGTACTATGCGGAGACCCCATGCA 3420
D 3361 GCGTTGTTGCTATCGTCAGAGCCCGCAAGAGGTAGTACTATGCGGAGACCCCATGCA 3420
Q 3421 TGGCGATTCTTCAACATGATGCACTAAAGTACATTTCAATCACCTGAAAAAGACATA 3480
D 3421 TGGCGATTCTTCAACATGATGCACTAAAGTACATTTCAATCACCTGAAAAAGACATA 3480
Q 3481 TGCACCAAGCATTTCTCAAGTATATCTCCGCGGTGCGACACAGCGATTAAGCTAATT 3540
D 3481 TGCACCAAGCATTTCTCAAGTATATCTCCGCGGTGCGACACAGCGATTAAGCTAATT 3540
Q 3541 GTATCGACATGCTTATGATGGAAGATGAAAAACAGAACCGGTGCAAGAAACATT 3600
D 3541 GTATCGACATGCTTATGATGGAAGATGAAAAACAGAACCGGTGCAAGAAACATT 3600

Q 3601 GAAATGATATTACAGGGGCAAAAGCCGAAGCCAGGGGATATCATCTGACATGTTTC 3660
D 3601 GAAATGATATTACAGGGGCAAAAGCCGAAGCCAGGGGATATCATCTGACATGTTTC 3660
Q 3661 CGCGGGTGGTTAAGCAATTGCAATTCGATCTATCCCGGACATGAAGTATGACCGCG 3720
D 3661 CGCGGGTGGTTAAGCAATTGCAATTCGATCTATCCCGGACATGAAGTATGACCGCG 3720
Q 3721 GCCTCAAGGGGTTAACGAAAGAGGTATGCGCTCCGGCAAAAGTCATGAAAAAC 3780
D 3721 GCCTCAAGGGGTTAACGAAAGAGGTATGCGCTCCGGCAAAAGTCATGAAAAAC 3780
Q 3781 CCACTGACGATCATCAAGCATGATGAACTGTGCTCAACCGCATGAGACAG 3840
D 3781 CCACTGACGATCATCAAGCATGATGAACTGTGCTCAACCGCATGAGACAG 3840
Q 3841 CTATGTTGAAAACTTGGACGGGCGACCATGATTAACACGCCCTAACTAACTAA 3900
D 3841 CTATGTTGAAAACTTGGACGGGCGACCATGATTAACACGCCCTAACTAACTAA 3900
Q 3901 GGAACCTTCAGGCTACTATAGAGACTGGAAGCTGAACAAAGGAATTAATTGCTGA 3960
D 3901 GGAACCTTCAGGCTACTATAGAGACTGGAAGCTGAACAAAGGAATTAATTGCTGA 3960
Q 3961 ATAAACAGCCCACTCCCGTCCCAATCCGTTACGCTGCAAGCAACGTTGCTGGCG 4020
D 3961 ATAAACAGCCCACTCCCGTCCCAATCCGTTACGCTGCAAGCAACGTTGCTGGCG 4020
Q 4021 AAAGCATTTGAACCGATTAACCAACGCGCGGTATGCTTAACCGGTGCGCATGAG 4080
D 4021 AAAGCATTTGAACCGATTAACCAACGCGCGGTATGCTTAACCGGTGCGCATGAG 4080
Q 4081 GAACTGTTCCCAAGTTTCCGATGACAAACCATTCGACCTTAACGCTTGAAGCTA 4140
D 4081 GAACTGTTCCCAAGTTTCCGATGACAAACCATTCGACCTTGAAGCTA 4140
Q 4141 ATTGCAATTAAGTTTTCGCAATGACCTTGAACAGCGACTGTTTCTAAACAGACATC 4200
D 4141 ATTGCAATTAAGTTTTCGCAATGACCTTGAACAGCGACTGTTTCTAAACAGACATC 4200
Q 4201 CCACTAAGCTACATCCCGCGCATTCAGAGAGCGGTAGCTCATTTGGGACAAACGCCA 4260
D 4201 CCACTAAGCTACATCCCGCGCATTCAGAGAGCGGTAGCTCATTTGGGACAAACGCCA 4260
Q 4261 GGAACCCGCAAGTATGGTACATCAAGCATTCGCGCGAACTCTCCGTAGATTCCG 4320
D 4261 GGAACCCGCAAGTATGGTACATCAAGCATTCGCGCGAACTCTCCGTAGATTCCG 4320
Q 4321 GTGTTCAAGCTAGCTGGAGAGGCAACAATTGATTTGCAACGCGGAGAAACAGATT 4380
D 4321 GTGTTCAAGCTAGCTGGAGAGGCAACAATTGATTTGCAACGCGGAGAAACAGATT 4380
Q 4381 ATCTCGCAACGATTAACCTGTCCTCGGGAACCGCACTCTCTCAACGCTTATGCCCC 4440
D 4381 ATCTCGCAACGATTAACCTGTCCTCGGGAACCGCACTCTCTCAACGCTTATGCCCC 4440
Q 4441 GAGTACAAGAGAAAGCAACCGCGCGGTCAAAAAATTTTGAACCAAGTTCAACACAC 4500
D 4441 GAGTACAAGAGAAAGCAACCGCGCGGTCAAAAAATTTTGAACCAAGTTCAACACAC 4500
Q 4501 TCAGTACTTGTGATCAAGAGAAAAAATTTGAAGCTCCCGTAAGAAATCGAATGATC 4560
D 4501 TCAGTACTTGTGATCAAGAGAAAAAATTTGAAGCTCCCGTAAGAAATCGAATGATC 4560
Q 4561 GCGCGATTTGGAATGCGCGGTGCAATTAAGAACTCAACCTGCTTCCGCTTCCGCG 4620
D 4561 GCGCGATTTGGAATGCGCGGTGCAATTAAGAACTCAACCTGCTTCCGCTTCCGCG 4620
Q 4621 CAGGCAAGTACGACCTGCTTCAATCAATTTGAACCTTAATACAGAAACCACTTT 4680
D 4621 CAGGCAAGTACGACCTGCTTCAATCAATTTGAACCTTAATACAGAAACCACTTT 4680

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DB 4741 TTAAACCTCAGGAGGACCCCTGCTGAGTCTATGAGCTTACCGCGACCGCAACAGTGG 4800
QY 4801 GAGCTAGTCAACCGCTCTTTCGAGAAAGTTTGTCAAGGCTGTGAGCGAGACAGATTTGT 4860
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QY 5041 GAAGCACTTGTCAACGCAACCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCTGCTG 5100
DB 5041 GAAGCACTTGTCAACGCAACCAATCCGCTGGGTAGACCAAGCGAAGAGTCTGCTGCTG 5100
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DB 5101 ATCTATTAACGTTTGGCGGACCAAGTTTAAACGATTCACCGACCGAGACAGGCAACGGCAAGA 5160
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DB 5161 ATGACTGTGCTCAGGAAAGAAAGTATCCACCGCGTGGCCCTGATTTCCGGAAGCAC 5220
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DB 5281 AATGAAACATAACATCAAGTCTGTGCGCAATTCACCTATCTAATGAGCATTTTACGAGCC 5340
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DB 5821 CTTAAGAGCAATTAACGTAAGAGTAAAGTATGAGTCTCTCTCCACACCCCTTCTTAAGCAC 5880
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DB 5941 CCGGCAATTCGTTCCCGCCCTTAAGTAACTGAAAGTGCAGAAACAGCTTACCGCTCTCCT 6000
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DB 6061 ACCTGCTGATGTCAAGACATCTCACTGATATGAGATGACAGTACGAAAGCTCACTT 6120
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DB 6121 TTTTTCAGCTTTTACCGGATGAGACACTTATTAATGATGACAGTGGTGTGACAGA 6180
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DB 6181 CTTAGTTCACTAGAGATGATGAGACCGGAGCAGGTGTGCTGCTGCTTACATGCGCTC 6240
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DB 6301 AGAAAGAGCCCACTCCACCGGACAGCATATGCTTGAATGCTTCCACTCTCTTTTGGT 6360
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DB 6361 GGGGTATCAATGTCCTCGGATCAATTTTGAAGGAGAGAGCGCGCGGCGAGCGGGA 6420
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DB 6421 CAACCCCTGCGCAACAGGCCCCAGAGATGCTATGCTTTCGAGATGTTTCCAGAGGA 6480
QY 6481 GAGATTGATGAGCTGAGCCGACAGATGTAAGTCCGAAACCCGCTGTTGGATCAATTT 6540
DB 6481 GAGATTGATGAGCTGAGCCGACAGATGTAAGTCCGAAACCCGCTGTTGGATCAATTT 6540
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DB 6601 AAGCAGAGAGTGAAGCAGAGAGAGAGAGTGAATCTGAATCTGAATCTGAATCTGAATCTGA 6660
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DB 6721 CAGCTTACAGAACCCGACTTGGAGCGCAATGCTCTGAAAGAAATTAATGAGCCGCTGCTC 6780
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DB 6781 GACACGTGAAAAGAGAAACAATCAAACTCAGGTACCAAGATGAGCCGAGGAGCCAAC 6840
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Dh 6841 AAAAGTAGTACAGTCTCGTAAAGTAGAAAAATAGAAAAGCCATTAACCACTGAGCGACTA 6900
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Dh 6901 CTGTGAGGACTACGACTGTATTAAGTCTGCGCAGATGACCCAGATGCTATTAAGATGACC 6960
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Qy 7021 GTAGTGTCTGTAAACAATCTGATGATGAGAACTATCCGACAGTAGATCTTATCAGATT 7080
Dh 7021 GTAGTGTCTGTAAACAATCTGATGATGAGAACTATCCGACAGTAGATCTTATCAGATT 7080
Qy 7081 ACTGACGAGTACGATGCTTACTTGTAGTAGAGACGACAGTGTGATGCTGATGATCT 7140
Dh 7081 ACTGACGAGTACGATGCTTACTTGTAGTAGAGACGACAGTGTGATGCTGATGATCT 7140
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Dh 7141 GCAACCTTTCTGCCCCGCTTAAGTGAAGTTAACCGAAAAACATGAGTATGAGCCCCG 7200
Qy 7201 AATATCCGAGTGGGCTTCATCAGCGATGCGAACAACGCTACAAAATGTGCTCATTTGCC 7260
Dh 7201 AATATCCGAGTGGGCTTCATCAGCGATGCGAACAACGCTACAAAATGTGCTCATTTGCC 7260
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Dh 7501 CCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7560
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Dh 7621 TACTTATGCGGATTCACCGGAAATTAAGTGTAGGCTTACCGGCGTCTTGTCTCCAAAC 7680
Qy 7681 ATTGACACGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7740
Dh 7681 ATTGACACGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 7740
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Dh 7741 AAGCAAGGCGACCGGCTACTGAGACCGGATATCGCATCTTTGCAAAAGCAAGAGAC 7800
Qy 7801 GCTATGCGCTTAACCGGCTGATGATCTTGAAGACCTGGGTGTGATCAACCACTACTC 7860
Dh 7801 GCTATGCGCTTAACCGGCTGATGATCTTGAAGACCTGGGTGTGATCAACCACTACTC 7860
Qy 7861 GACTGTATGAGAGCGGCTTTGAGAAATATCAATCCCATCTTAAGGCTGATCTGCT 7920
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Qy 7921 TTTAAATTCGGGCGATGATGAAATCCGAAATGTTCTCTCACTTTTGTCAACACAGTT 7980
Dh 7921 TTTAAATTCGGGCGATGATGAAATCCGAAATGTTCTCTCACTTTTGTCAACACAGTT 7980

Qy 7981 TTGAATGCTGTTATTCGCCAGCAGATGATGAAAGACGGCTTAAACGTCACAGATGCA 8040
Dh 7981 TTGAATGCTGTTATTCGCCAGCAGATGATGAAAGACGGCTTAAACGTCACAGATGCA 8040
Qy 8041 GCGTTACTTGGGCGACGACATCATATCATGAGTATGATGATGATGATGATGATGATGATG 8100
Dh 8041 GCGTTACTTGGGCGACGACATCATATCATGAGTATGATGATGATGATGATGATGATGATG 8100
Qy 8101 AGGTGCGCCACCTGGCTCAACATGAGGTTAAGATCATGACGACATCATCGGTGAGAG 8160
Dh 8101 AGGTGCGCCACCTGGCTCAACATGAGGTTAAGATCATGACGACATCATCGGTGAGAG 8160
Qy 8161 CCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGTTACTTCCACAGGTCGCG 8220
Dh 8161 CCACTTACTTCTGCGCGGATTTATCTTGCAAGATTCGTTACTTCCACAGGTCGCG 8220
Qy 8221 GTGGCGGATCCCTGAAAAAGGCTTTAAAGTTGGTAAACCGCTCCAGCGACGAG 8280
Dh 8221 GTGGCGGATCCCTGAAAAAGGCTTTAAAGTTGGTAAACCGCTCCAGCGACGAG 8280
Qy 8281 CAAGACGAAGACGAAGACGCGCTGCTAGATGAAACAAAGCGGTTTGAAGAGGT 8340
Dh 8281 CAAGACGAAGACGAAGACGCGCTGCTAGATGAAACAAAGCGGTTTGAAGAGGT 8340
Qy 8341 ATTAACGAGCACTTTAGCAGTGGCGGTGACGACCCGCTATGAGGTAGACATATTACACT 8400
Dh 8341 ATTAACGAGCACTTTAGCAGTGGCGGTGACGACCCGCTATGAGGTAGACATATTACACT 8400
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Dh 8401 GTCTTACTGCGATTTGAAACTTTTGCCGAGCAAAAGCATTTCCAAAGCATCAGAGG 8460
Qy 8461 GAAATTAAGCATCTACGCGTGGTCTTAATATGTCAGCATAGTATTCATCTGACTAA 8520
Dh 8461 GAAATTAAGCATCTACGCGTGGTCTTAATATGTCAGCATAGTATTCATCTGACTAA 8520
Qy 8521 TACTACACACCAACCACT 8539
Dh 8521 TACTACACACCAACCACT 8539

RESULT 4
ADL71889
ID ADL71889 standard; cDNA; 11282 BP.
XX
XX ADL71889;
AC
XX 20-MAY-2004 (first entry)
DT
DE Temperature inducible alphavirus vector pCyt5.
XX
XX Gene expression; vector; pCyt5; ss.
XX
XX Rous sarcoma virus.
OS Alphavirus.
OS Chimeric.
XX
XX MO2004018506-A2.
PN
XX
XX PD 04-MAR-2004.
XX
XX PF 21-AUG-2003; 2003WO-BP009291.
XX
XX PR 22-AUG-2002; 2002US-0404928P.
XX
XX PR 11-DEC-2002; 2002US-0432259P.
XX
XX PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
PI Ivanova L, Renner WA, Saudan P;
XX WPI; 2004-226795/21.
XX

PT New nucleic acid molecule comprising first, second and third
PT polypeptide elements, useful for regulating the expression of a
XX polypeptide or an untranslated RNA molecule.

PS Example 1; SEQ ID NO 1; 112bp; English.

XX The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCYTs containing a Rous sarcoma
CC virus (RSV) promoter. The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic
CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin orip and the cis- or trans-
CC acting gene product EBNA-1, with pCYTs ADL71909-ADL71910. Due to the
CC presence of orip and EBNA-1, the novel vector is maintained episomally in
CC the form of several DNA copies in cell nuclei. These multiple DNA copies
CC may be transcribed from the RSV promoter into Cyts RNA replicons, but
CC remain inactive unless cells are shifted to a certain temperature. Only
CC after temperature induction does replicon replication occur, followed by
CC RNA accumulation and translation in the cell cytoplasm, and production of
CC the polypeptide of interest.

XX Sequence 11282 BP; 3152 A; 2821 C; 2767 G; 2542 T; 0 U; 0 Other;

Query Match 100.0%; Score 8539; DB 12; Length 11282;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Gaps 0;

Matches 8539; Conservative 0; Indels 0; Gaps 0;

QY 1 CTGACGGCCCTGTAGCGGCATTAAGCGCGGGGTGTGTGTTACGCGACGCTGA 60
DB 1 CTGACGGCCCTGTAGCGGCATTAAGCGCGGGGTGTGTGTTACGCGACGCTGA 60
QY 61 CCGCTACATTGCCAGCGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCG 120
DB 61 CCGCTACATTGCCAGCGCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCCTTCCG 120
QY 121 CCAGCTTCGCGCGGCTTCCCGGTCAAGCTTAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
DB 121 CCAGCTTCGCGCGGCTTCCCGGTCAAGCTTAATCGGGGGCTCCCTTTAGGGTTCCGAT 180
QY 181 TTATGCTTTTACGCGACCTCGACCCCAAAAACCTTGATTTAGGTGATGCTCAGTATG 240
DB 181 TTATGCTTTTACGCGACCTCGACCCCAAAAACCTTGATTTAGGTGATGCTCAGTATG 240
QY 241 GGCCATGCGCTGTATGACGCGTTCCTTTGCGCTTTGAGCTTGGAGTCCAGTTCCTTAATA 300
DB 241 GGCCATGCGCTGTATGACGCGTTCCTTTGCGCTTTGAGCTTGGAGTCCAGTTCCTTAATA 300
QY 301 GTGACCTTGTTCCTCAAACTGGAACAACATCAACCCATCTCGCTATCTTTGATT 360
DB 301 GTGACCTTGTTCCTCAAACTGGAACAACATCAACCCATCTCGCTATCTTTGATT 360
QY 361 TATAAGGATTTTCCGCTATTTGCGCTATTTGTTTAAATGAGCTGATTTAAACAAAAT 420
DB 361 TATAAGGATTTTCCGCTATTTGCGCTATTTGTTTAAATGAGCTGATTTAAACAAAAT 420
QY 421 TTAACGGCAATTTTAACAAAATATTAACGTTAACAATTCATTTCGCAATTCAGGCTGCG 480
DB 421 TTAACGGCAATTTTAACAAAATATTAACGTTAACAATTCATTTCGCAATTCAGGCTGCG 480

DB 421 TTAACGGCAATTTTAACAAAATATTAACGTTAACAATTCATTTCGCAATTCAGGCTGCG 480
QY 481 CAATGTTGGAGAGGGGATCGGTGCGGGCTCTTCGCTATTAAGCGAGCTGGGAAAG 540
DB 481 CAATGTTGGAGAGGGGATCGGTGCGGGCTCTTCGCTATTAAGCGAGCTGGGAAAG 540
QY 541 GGGATGCTGCAAGGCGATTAAGTTGGGTACCGCAAGGTTTCCAGTACGACGTTG 600
DB 541 GGGATGCTGCAAGGCGATTAAGTTGGGTACCGCAAGGTTTCCAGTACGACGTTG 600
QY 601 TAAACGACGGCCGATGAGCGCCGCAATTAACCTTCAATTAAGGAAACAAAAGCTGGCTAG 660
DB 601 TAAACGACGGCCGATGAGCGCCGCAATTAACCTTCAATTAAGGAAACAAAAGCTGGCTAG 660
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DB 661 TGATTCAGCTTTATGCAATCTCTTGTAGCTTGCACATGTGTAAGATGATTAGCA 720
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DB 721 CATGCTTTACAGGAGAGAAAAGACCGTGCATGCGGATTTGTGAAAGTAAAGTGTAC 780
QY 781 GATGTCCTTTATGAGAGGCAACAGCGGCTGTGACATGATTTGAGCAACCACTGAA 840
DB 781 GATGTCCTTTATGAGAGGCAACAGCGGCTGTGACATGATTTGAGCAACCACTGAA 840
QY 841 TTCCGCAATTCAGAGATATTGATTTTAAAGTCCCTACCTGATACCGTGCAGATTGACGG 900
DB 841 TTCCGCAATTCAGAGATATTGATTTTAAAGTCCCTACCTGATACCGTGCAGATTGACGG 900
QY 901 CGTAGTACACATTTAATTAATCAACCGGACCAATTCAGTACATCAATGAGAGAG 960
DB 901 CGTAGTACACATTTAATTAATCAACCGGACCAATTCAGTACATCAATGAGAGAG 960
QY 961 CCACTAGTAAACGTAGACGTAGACCCCAAGTCCGTTGTGCTGCACTGCAAAAGC 1020
DB 961 CCACTAGTAAACGTAGACGTAGACCCCAAGTCCGTTGTGCTGCACTGCAAAAGC 1020
QY 1021 TTCCGCAATTCAGAGATATTGATTTTAAAGTCCCTACCTGATACCGTGCAGATTGACGG 1080
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QY 1081 GCATTTTCGATCTGCGCAGTAACTAATCGAGCTGAGGTTCTTCAACACGACGATC 1140
DB 1081 GCATTTTCGATCTGCGCAGTAACTAATCGAGCTGAGGTTCTTCAACACGACGATC 1140
QY 1141 TTGACATPAGGACGCGACCGGCTGTGAAATGTTTCCGAGCACCACTATCTGTGTC 1200
DB 1141 TTGACATPAGGACGCGACCGGCTGTGAAATGTTTCCGAGCACCACTATCTGTGTC 1200
QY 1201 TGCCCATGCGGTGTCCAGAAAGACCGGACCGCATGTGAATPAGGCAATGAACTGGCG 1260
DB 1201 TGCCCATGCGGTGTCCAGAAAGACCGGACCGCATGTGAATPAGGCAATGAACTGGCG 1260
QY 1261 GAAACGCTGCAAGATTTAACAACAGAACTTGATGAGAAATTAAGATTCGCGAGC 1320
DB 1261 GAAACGCTGCAAGATTTAACAACAGAACTTGATGAGAAATTAAGATTCGCGAGC 1320
QY 1321 GTACTTATATGCGCGGATGCTGAAACACATCGCTGCTTTCACAAAGATTTACTGC 1380
DB 1321 GTACTTATATGCGCGGATGCTGAAACACATCGCTGCTTTCACAAAGATTTACTGC 1380
QY 1381 AACATGGGTCCGAATTTCCGCTATGACAGAGGTATTAACAGCTCCCGGAATATC 1440
DB 1381 AACATGGGTCCGAATTTCCGCTATGACAGAGGTATTAACAGCTCCCGGAATATC 1440
QY 1441 TATCATCAGGCTATGAAAGGCTGCGGACCTGTACTGATTTGCTTGCACACCAACCCAG 1500
DB 1441 TATCATCAGGCTATGAAAGGCTGCGGACCTGTACTGATTTGCTTGCACACCAACCCAG 1500
QY 1501 TTCAATGTTCTCGGCTATGAGGAGGTTGATCCCTGCTGTAACAACCACTGGGCGAGAG 1560
DB 1501 TTCAATGTTCTCGGCTATGAGGAGGTTGATCCCTGCTGTAACAACCACTGGGCGAGAG 1560

QY 1561 AAAGCTTGAAGCGCGTAACATCGGACTTTGACAGCAAAAGCTGAGTAAGTAGACA 1620
Db 1561 AAAGCTTGAAGCGCGTAACATCGGACTTTGACAGCAAAAGCTGAGTAAGTAGACA 1620
QY 1621 GGAATAATGTGATTAATGAGAAAGAAAGTTGAAGCCCGGGTGGGGTTATTTCTCC 1680
Db 1621 GGAATAATGTGATTAATGAGAAAGAAAGTTGAAGCCCGGGTGGGGTTATTTCTCC 1680
QY 1681 GTAGAGTGCACATTTATCCAGAACACAGAGCCAGCTTGACAGCTGGCATCTTCCATCG 1740
Db 1681 GTAGAGTGCACATTTATCCAGAACACAGAGCCAGCTTGACAGACTGGCATCTTCCATCG 1740
QY 1741 GTGTTCCATCTTGAATGGAAGCAGTCGTAACATTTGCGCGCTGTGATPAOAGTGTGAGTTGC 1800
Db 1741 GTGTTCCATCTTGAATGGAAGCAGTCGTAACATTTGCGCGCTGTGATPAOAGTGTGAGTTGC 1800
QY 1801 GAAGGCTACGTAGTGAAGAAATACCATCGATCCCGGGATCAAGGAGAAACCGTGGGA 1860
Db 1801 GAAGGCTACGTAGTGAAGAAATACCATCGATCCCGGGATCAAGGAGAAACCGTGGGA 1860
QY 1861 TACGCGGTTACACAAATAGCGAGGCGTTCTTGCTATGCAAAAGTTACTGACACAGTAAAA 1920
Db 1861 TACGCGGTTACACAAATAGCGAGGCGTTCTTGCTATGCAAAAGTTACTGACACAGTAAAA 1920
QY 1921 GGAAGACGGGTATGTTCTCTGTGTGACGTACATCCCGGCAACATATGCGATCAGATG 1980
Db 1921 GGAAGACGGGTATGTTCTCTGTGTGACGTACATCCCGGCAACATATGCGATCAGATG 1980
QY 1981 ACTGATTAATGAGCGAGATATATCATCTGACGATGACAAAACCTTGGTGGGCTC 2040
Db 1981 ACTGATTAATGAGCGAGATATATCATCTGACGATGACAAAACCTTGGTGGGCTC 2040
QY 2041 AACGAGGAAATTTGCTATTAACGATAGGACTPAACAGAAACCAACACATGCAAAATTAC 2100
Db 2041 AACGAGGAAATTTGCTATTAACGATAGGACTPAACAGAAACCAACACATGCAAAATTAC 2100
QY 2101 CTTTGGCCGATCATAGACCAAGGCTTCAAGCAATGGGCTAAGAGCGGCAAGATGATCTT 2160
Db 2101 CTTTGGCCGATCATAGACCAAGGCTTCAAGCAATGGGCTAAGAGCGGCAAGATGATCTT 2160
QY 2161 GATTAACAGAAATGCTGGGATCTAGAGAAAGCAAGGCTTACGTATGGCTGTGGGCG 2220
Db 2161 GATTAACAGAAATGCTGGGATCTAGAGAAAGCAAGGCTTACGTATGGCTGTGGGCG 2220
QY 2221 TTTCGCACTAAGAAAGTACATTCGTTTATCGCCACCTGGAAGCGACAGCCTGGTAAAA 2280
Db 2221 TTTCGCACTAAGAAAGTACATTCGTTTATCGCCACCTGGAAGCGACAGCCTGGTAAAA 2280
QY 2281 GTCCAGCCTCTTTAGCGCTTTTCCCATGTCGTCGCTATGAGAGCACTCTTGGCCATG 2340
Db 2281 GTCCAGCCTCTTTAGCGCTTTTCCCATGTCGTCGCTATGAGAGCACTCTTGGCCATG 2340
QY 2341 TCGCTGAGGAGAAATGAAACTGCGCATTCGCAACCAAGAGAGAGAAAACTGCTGAG 2400
Db 2341 TCGCTGAGGAGAAATGAAACTGCGCATTCGCAACCAAGAGAGAGAAAACTGCTGAG 2400
QY 2401 GTCTCGAGAGATTAATGATAGAGAGCGCAAGGCTGCTTTAGAGATGCTCAGAGAAAGCC 2460
Db 2401 GTCTCGAGAGATTAATGATAGAGAGCGCAAGGCTGCTTTAGAGATGCTCAGAGAAAGCC 2460
QY 2461 AGAGCGGAGAAAGCTCGAGAAAGCACTTCCACATTAATGAGCAACAAAGCATTCAGAGCA 2520
Db 2461 AGAGCGGAGAAAGCTCGAGAAAGCACTTCCACATTAATGAGCAACAAAGCATTCAGAGCA 2520
QY 2521 GCGCGAGAAATTTGCTGCGAAGTGAAGGAGCTCCAGGCGGACATCGGAGAGCATTAAGTT 2580
Db 2521 GCGCGAGAAATTTGCTGCGAAGTGAAGGAGCTCCAGGCGGACATCGGAGAGCATTAAGTT 2580
QY 2581 GAAACCCCGCGGCTCAGTAAGATTAATCTTCAAGCAAAATGACCGTATGATCGAGCAG 2640
Db 2581 GAAACCCCGCGGCTCAGTAAGATTAATCTTCAAGCAAAATGACCGTATGATCGAGCAG 2640

QY 2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGATGCCAAACTCGCACCGACGCCG 2700
Db 2641 TATATCGTTGTCTCGCCAAACTCTGTGCTGAAGATGCCAAACTCGCACCGACGCCG 2700
QY 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGGTAACGGGTGAA 2760
Db 2701 CTAGCAGATCAGGTTAAGATCATTAACAACCTCCGGAAGATCAGGAAGGTAACGGGTGAA 2760
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Db 2761 CCATACGAGCTTAAATGATGATGAGCAGAGAGAGTCCGTACATGCGCAGAAATTCCTA 2820
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Db 2821 GCACTAGTAGAGCGCCACGTTATGTTAACAAGAAAGAGATTGTGAACCGCAAACTA 2880
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Db 3121 GTGATAGGACACCGGGGTCGGGCAAGTCAGCTATTAATGAATCAACTGTCAACGACAGA 3180
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Db 3301 AAAGCGGTAAAGTGCTGATCTTGAAGAGCGTTCCGCTGCGACAGCAGACACTACTT 3360
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QY 3541 GTATGACATCTGATTAAGATGAAAGATGAAGAACCAAGAACCCGTGCAAGAAAGACAT 3600
Db 3541 GTATGACATCTGATTAAGATGAAAGATGAAGAACCAAGAACCCGTGCAAGAAAGACAT 3600
QY 3601 GAAATCGATTAACAGGGGCGCAAGAGCGAAGCGCAGGGGATATCATCTGACATGTTTC 3660
Db 3601 GAAATCGATTAACAGGGGCGCAAGAGCGAAGCGCAGGGGATATCATCTGACATGTTTC 3660
QY 3661 GCGGGGTGGGTTAAGCAATTCGAAATCGACTATCCCGGACATGAAGTATGACAGCGCG 3720
Db 3661 GCGGGGTGGGTTAAGCAATTCGAAATCGACTATCCCGGACATGAAGTATGACAGCGCG 3720
QY 3721 GCCTCAAGAGGCTTAACCAAGAAAGAGATGATGCGCGTCCGCAAAAAGTCAATGAAAC 3780

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Db 3721 GCGCTCAAGAGGCTTACAGAAAAAGAGTGTATCCGTCGCGCAAAAAAGTCAAGAAAAAC 3780
Qy 3781 CCACTGTACGGGATCATCATGAGCATGTGAACGNTGTCTCACCCGATGAGACAGG 3840
Db 3781 CCACTGTACGGGATCATCATGAGCATGTGAACGNTGTCTCACCCGATGAGACAGG 3840
Qy 3841 CTAGTGTGAAAAACCTTGCAGAGGCGACCATGATTAAGCAGCCCACTAACATCTTAA 3900
Db 3841 CTAGTGTGAAAAACCTTGCAGAGGCGACCATGATTAAGCAGCCCACTAACATCTTAA 3900
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Db 3901 GGAACCTTTCAAGGCTACTATAGAGACTGGGAAGCTGAACAGAGGAATATTGCTGCA 3960
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Db 3961 ATTAAGCCCCCACTCCCGGCAATCCGTTACGCTGCAAGCAACGTTTGTGGGCG 4020
Qy 4021 AAGACATTGGAACCGATCTAGCAAGCGCCGGTATCGTACTTAACGGTTGCAAGTGAAGC 4080
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Qy 5461 CAATTAAGAGTCTGTACAGAGCTGAGAGTGAAGATTAAGAGATGAGATGAGATGTA 5520
Db 5461 CAATTAAGAGTCTGTACAGAGCTGAGAGTGAAGATTAAGAGATGAGATGAGATGTA 5520
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Db 5581 AAATTTGATTCGTAATTCGAAAGGACCAAAATTCATCAAGCAGAGAAAGATGCGGAG 5640
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Db 5701 GGTGAGACATGGAAGCAATCCGGAAGAGTCCCGGTGACATCAACCCGTCGTAGC 5760
Qy 5761 CCGGCCAAAACGTTGCGGTGCTTGAATGTATGACATGACGCGCAAGAAAGGTCACAGA 5820
Db 5761 CCGGCCAAAACGTTGCGGTGCTTGAATGTATGACATGACGCGCAAGAAAGGTCACAGA 5820
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Db 5821 CTTAGAGCAATAAGTCAAGAAAGTATCAGTATGCTCTCTCAACCCCTTCTTAAGCAC 5880
Qy 5881 AAAATTAAGAAATGTTCAAGAAAGTTCAAGTGAAGAAAGTGTCTGTTAATCCGACACT 5940
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QY	5941	CCCGCATTCGTTCCCGCCCGTAAAGTACATAGAAAGTCCAGAAACAGCTTACCGCTCTCTCT	6000
Db	5941	CCCGCATTCGTTCCCGCCCGTAAAGTACATAGAAAGTCCAGAAACAGCTTACCGCTCTCTCT	6000
QY	6001	GCACAGGCCGAGAGAGGCCCCGAAATTGAGGACACCGTCAACCACTTCAAGCTGATAC	6060
Db	6001	GCACAGGCCGAGAGAGGCCCCGAAATTGAGGACACCGTCAACCACTTCAAGCTGATAC	6060
QY	6061	ACCTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAGGCTCACTT	6120
Db	6061	ACCTCGCTTGATGTCAAGACATCTCACTGGATATGATGACAGTAGCGAAGGCTCACTT	6120
QY	6121	TTTTCGACCTTTAGGGGATTCGGACAACTCTATTTACTATTAATGACACATTTGGTTCGACGA	6180
Db	6121	TTTTCGACCTTTAGGGGATTCGGACAACTCTATTTACTATTAATGACAGTTGGTTCGACGA	6180
QY	6181	CCTAGTTCATAGAGATAGTAGACCGGAAGGCGAGGTGTGTGTGGCTGACGTTCAATGCGCT	6240
Db	6181	CCTAGTTCATAGAGATAGTAGACCGGAAGGCGAGGTGTGTGTGGCTGACGTTCAATGCGCT	6240
QY	6241	CAAGAGCTGCCCTTATTTCCACCGCCAAAGCTAAAGAAATGGCCCGCTTGGCAGCGCA	6300
Db	6241	CAAGAGCTGCCCTTATTTCCACCGCCAAAGCTAAAGAAATGGCCCGCTTGGCAGCGCA	6300
QY	6301	AGAAAAGAGCCCATCTCCACCGGCAAGCAATAGCTGTGATCCCTCAACTCTCTTTTGGT	6360
Db	6301	AGAAAAGAGCCCATCTCCACCGGCAAGCAATAGCTGTGATCCCTCAACTCTCTTTTGGT	6360
QY	6361	GGGGTATCCATGTCCCTCGGATCAATTTTTCAGCGAGAGACGGCCCGCAGGACCGGTA	6420
Db	6361	GGGGTATCCATGTCCCTCGGATCAATTTTTCAGCGAGAGACGGCCCGCAGGACCGGTA	6420
QY	6421	CAACCCCTGGGAAACAGGGCCCAACGGAATGGTCCCTATGCTTCGATGCTTTTCCGACGGA	6480
Db	6421	CAACCCCTGGGAAACAGGGCCCAACGGAATGGTCCCTATGCTTCGATGCTTTTCCGACGGA	6480
QY	6481	GAGATTGATGAGCTGAGGCGGACAGTAATCTGATGCCAACCCTGCTGTTTGGATCAATTT	6540
Db	6481	GAGATTGATGAGCTGAGGCGGACAGTAATCTGATGCCAACCCTGCTGTTTGGATCAATTT	6540
QY	6541	GAACCCGGGCGAAGTGAATCTCAATTAATACGTCGATACGCCGATCTTTTCCACTACGC	6600
Db	6541	GAACCCGGGCGAAGTGAATCTCAATTAATACGTCGATACGCCGATCTTTTCCACTACGC	6600
QY	6601	AAGCAGAACCTTAGACGAGAGACGAGAGACTGAATCTCACTAATCCGGGGTATGATGGG	6660
Db	6601	AAGCAGAACCTTAGACGAGAGACGAGAGACTGAATCTCACTAATCCGGGGTATGATGGG	6660
QY	6661	TACATATTTTCGACGGACACAGGCCCTTGGGCACTTGCMAAAGAAATCCGTTCTTCAGAAC	6720
Db	6661	TACATATTTTCGACGGACACAGGCCCTTGGGCACTTGCMAAAGAAATCCGTTCTTCAGAAC	6720
QY	6721	CAGCTTACAGAACCGAAGCTTGGAGGGCAATGCTCCGAAABAATTCATGCCCGGATGCTC	6780
Db	6721	CAGCTTACAGAACCGAAGCTTGGAGGGCAATGCTCCGAAABAATTCATGCCCGGATGCTC	6780
QY	6781	GACACGTGAAAGAGGAACTCACTCAATCTCAGTACACAGATGATGCCACCGAAGCCAAC	6840
Db	6781	GACACGTGAAAGAGGAACTCACTCAATCTCAGTACACAGATGATGCCACCGAAGCCAAC	6840
QY	6841	AAAAGTAGTACCACTCTCTGTTAAAGTAGAAAATCAGAAAGCCATTAACCACTGACGCACTA	6900
Db	6841	AAAAGTAGTACCACTCTCTGTTAAAGTAGAAAATCAGAAAGCCATTAACCACTGACGCACTA	6900
QY	6901	CTGTACAGACATACGACTGTATATCTCTGACACAGATCAGCAGAAATGCTATTAAGTCAAC	6960
Db	6901	CTGTACAGACATACGACTGTATATCTCTGACACAGATCAGCAGAAATGCTATTAAGTCAAC	6960
QY	6961	TATCCGAAACCATTTGATCTCCAGTAGGCTACCGCGAACTATCTCCGATCCACAGTTGCT	7020
Db	6961	TATCCGAAACCATTTGATCTCCAGTAGGCTACCGCGAACTATCTCCGATCCACAGTTGCT	7020

QY	7021	GTAGTGTCTGTAAACAACTATCTGATGAGAACTATCCGACAGTATGCACTTTATACAGATT	708
Db	7021	GTAGTGTCTGTAAACAACTATCTGATGAGAACTATCCGACAGTATGCACTTTATACAGATT	708
QY	7081	ACTGACGATGACGATGCTTACTTGATATGATGATACGACGACGTGCGTCTGATATCT	714
Db	7081	ACTGACGATGACGATGCTTACTTGATATGATGATACGACGACGTGCGTCTGATATCT	714
QY	7141	GCAACCTTCTGCCCCGCTTAAGCTTAGAATTACCCGAAAAACATGAGTATGAGCCCCG	7200
Db	7141	GCAACCTTCTGCCCCGCTTAAGCTTAGAATTACCCGAAAAACATGAGTATGAGCCCCG	7200
QY	7201	AATATCCGACGTGCGGTTCCATGCGGATGAGAAACGCTACAAAATGTGCTCATTTGCC	7266
Db	7201	AATATCCGACGTGCGGTTCCATGCGGATGAGAAACGCTACAAAATGTGCTCATTTGCC	7266
QY	7261	GCAACTAAAGAAATTGCAACGTCACGCGAGTGGTGAATGCCAACCTGGACTGACGCG	7320
Db	7261	GCAACTAAAGAAATTGCAACGTCACGCGAGTGGTGAATGCCAACCTGGACTGACGCG	7320
QY	7321	ACATTCGAATGTCGAATGCTTTCCGAATATGCAATGTAATGACGATATGGAGAGATTC	7380
Db	7321	ACATTCGAATGTCGAATGCTTTCCGAATATGCAATGTAATGACGATATGGAGAGATTC	7380
QY	7381	GCTCGGAAGCCAAATTAGATATCACCTAGATTTTGCACCGCATATGTAGCTAGACTGAA	7440
Db	7381	GCTCGGAAGCCAAATTAGATATCACCTAGATTTTGCACCGCATATGTAGCTAGACTGAA	7440
QY	7441	GGCCCTTAAGGCGCGCGCACTATTTTGCAAAACGTATTAATTTGGTCCCATTTGCAAAAGTG	7500
Db	7441	GGCCCTTAAGGCGCGCGCACTATTTTGCAAAACGTATTAATTTGGTCCCATTTGCAAAAGTG	7500
QY	7501	CCTATGATATGATTGCTCATGTGACATGAAAAAGACGTGAAAGTTTACACGACGACGAAA	7560
Db	7501	CCTATGATATGATTGCTCATGTGACATGAAAAAGACGTGAAAGTTTACACGACGACGAAA	7560
QY	7561	CACACAGAGAAAGACGGAAGTACAGATGATACAGCCGCGAAGACCCCTGGCGACTGCT	7620
Db	7561	CACACAGAGAAAGACGGAAGTACAGATGATACAGCCGCGAAGACCCCTGGCGACTGCT	7620
QY	7621	TACTTATGCGGGATTCAACCGGGAAATTATGTCGGTATGCGGCGCTTGCTTCCAAAC	7680
Db	7621	TACTTATGCGGGATTCAACCGGGAAATTATGTCGGTATGCGGCGCTTGCTTCCAAAC	7680
QY	7681	ATTCAACGCTTTTGAATGTGCGGCGAGGATTTTATGCAATCATAGCAAGCACTTC	7740
Db	7741	AAGCAAGGCGACCCGGTATCTGGAACCGGATATGCAATCATTCGACAAAGCCAAAGACGAC	7800
QY	7801	GCTATGCGGTTAACCGGTCGTATGATTTGGAGACCTGGGGTGTGATCAACCACTACTC	7860
Db	7801	GCTATGCGGTTAACCGGTCGTATGATTTGGAGACCTGGGGTGTGATCAACCACTACTC	7860
QY	7861	GACTTGATTCGAGTGGCGCTTTGGGAAATATCATCCCACTTACCTTACGGGATCTCGT	7920
Db	7921	TTTAAATTCGGGGGCGATGATGAATCCGGAATGTTCTCAACTTTTGTGACACAGTT	7980
QY	7981	TTGAATGTGCTTATCGCCACAGAGTACTTGAAGAGCGGCTTAAACGTCAGATGTGCA	8040
Db	8041	GCGTTCAATGGCGACGCAACATCATATCAATGAGTATATCTGCAAAAGAAATGGCTGAG	8100
QY	8101	AGGTGCGCCACCTGGCTCAACATGAGAGGTTAAGTATCTGACGCAAGTCACTCGGTGAGAGA	8160

Db 8101 AGGTGCGCCACCTGGCTCAACATGAGATTAAAGTCAATCGACGATCATCGTGAAGAGA 8160
Qy 8161 CCACCTTACTTCTGCGGGGATTTATCTGTGCAAGATTGCTTACTTCCACAGCGTGGCGC 8220
Db 8161 CCACCTTACTTCTGCGGGGATTTATCTGTGCAAGATTGCTTACTTCCACAGCGTGGCGC 8220
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Qy 8461 GAAATTAAGCATCTCTACGGTGTCTTAATATGTCAGCATAGTACATTCTGACTAA 8520
Db 8461 GAAATTAAGCATCTCTACGGTGTCTTAATATGTCAGCATAGTACATTCTGACTAA 8520
Qy 8521 TACTACAAACACCAACCACT 8539
Db 8521 TACTACAAACACCAACCACT 8539

RESULT 5

ID ADL71890 standard; cDNA; 13068 BP.
XX ADL71890;
AC ADL71890;
XX 20-MAY-2004 (first entry)
DT 20-MAY-2004 (first entry)
DE Temperature Inducible alphavirus vector pCyt2.1.
XX Gene expression; vector; pCyt2.1; ss.
KM Gene expression; vector; pCyt2.1; ss.
XX Cytomegalovirus.
OS Alphavirus.
OS Chimeric.
XX MO2004018506-A2.
PN 04-MAR-2004.
PD 04-MAR-2004.
XX 21-AUG-2003; 2003WO-EP009291.
PF 21-AUG-2003; 2003US-0404928P.
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX (CYTO-) CYTOS BIOTECHNOLOGY AG.
PA Ivanova L, Renner WA, Saudan P;
XX Ivanova L, Renner WA, Saudan P;
PI WPI; 2004-226795/21.
DR WPI; 2004-226795/21.
XX New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX Example 1; SEQ ID NO 2; 112bp; English.
XX The present sequence is that of the tightly regulated temperature
CC inducible alphavirus expression system pCyt2.1 containing a
CC cytomagalovirus (CMV). The vector can be used to drive transcription of
CC mRNA from a nucleic acid molecule of the invention. A claimed nucleic

CC acid molecule comprises: (A) a first polynucleotide element which encodes
CC an RNA molecule comprising (a) at least one cis-acting sequence element,
CC (b) a first nucleotide sequence comprising a first open reading frame,
CC the first open reading frame having a nucleotide sequence encoding an RNA
CC -dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, i.e. the cis-acting replication origin oriP and the cis or trans-
CC acting gene product EBNA-1 with pCyt2.1. Due to the presence of OriP and
CC EBNA-1, the novel vector is maintained episomally in the form of several
CC DNA copies in cell nuclei. These multiple DNA copies may be transcribed
CC from the CMV promoter into Cyt2.1 RNA replicons, but remain inactive
CC unless cells are shifted to a certain temperature. Only after temperature
CC induction does replicon replication occur, followed by RNA accumulation
CC and translation in the cell cytoplasm, and production of the polypeptide
CC of interest.

SO Sequence 13068 BP; 3555 A; 3379 C; 3204 G; 2930 T; 0 U; 0 Other;

Query Match 89.7%; Score 7657.2; DB 12; Length 13068;

Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 893 ATTGAGCGGCTAGACACATTTGATCAACAGCGGCAACATTTGACTACATCAACA 952
Db 869 ATTGAGCGGCTAGACACATTTGATCAACAGCGGCAACATTTGACTACATCAACA 928
Qy 953 TGGAGAAAGCAGTAGTAAGAGTAGACAGCCCGAGAGTCCGTTGTGCTGCACTGC 1012
Db 929 TGGAGAAAGCAGTAGTAAGAGTAGACAGCCCGAGAGTCCGTTGTGCTGCACTGC 988
Qy 1013 AAAAAAGCTTCCGCAATTTGAGTAGTAGACAGAGGTCTACTCCAAATGACATGCTA 1072
Db 989 AAAAAAGCTTCCGCAATTTGAGTAGTAGACAGAGGTCTACTCCAAATGACATGCTA 1048
Qy 1073 ATGCCAAGCATTTTCCCATCTGCGCCAGTAACCTAATCGAGCTGGAAGTCCATCCACAG 1132
Db 1049 ATGCCAAGCATTTTCCCATCTGCGCCAGTAACCTAATCGAGCTGGAAGTCCATCCACAG 1108
Qy 1133 CGACGATCTTGAGACATGAGCGCACCGGCTCGTAGAATGTTTCCGAGACACAGATATC 1192
Db 1109 CGACGATCTTGAGACATGAGCGCACCGGCTCGTAGAATGTTTCCGAGACACAGATATC 1168
Qy 1193 ATTGTGTCTGCCCATCGATGTCAGAGAAGCCGGAACCGCATGATGAATATGCCAGATA 1252
Db 1169 ATTGTGTCTGCCCATCGATGTCAGAGAAGCCGGAACCGCATGATGAATATGCCAGATA 1228
Qy 1253 AACTGGCGGAAAAAGCGTGCAGATTACAAACAAGAACTTGCAAGAGAATTAAGATC 1312
Db 1229 AACTGGCGGAAAAAGCGTGCAGATTACAAACAAGAACTTGCAAGAGAATTAAGATC 1288
Qy 1313 TCCGGAACGTAATGATACGCGGATGCTGAAACACCATGCTGCTTTCAACAAGATG 1372
Db 1289 TCCGGAACGTAATGATACGCGGATGCTGAAACACCATGCTGCTTTCAACAAGATG 1348
Qy 1373 TTACTCTCAACATGCGTCCGAATATTTCCGTATGAGAGAGTATATCAAGCTCCCG 1432
Db 1349 TTACTCTCAACATGCGTCCGAATATTTCCGTATGAGAGAGTATATCAAGCTCCCG 1408
Qy 1433 GAATATCTATCATCAGGCTATGAAGCGTGGCGGACCTGTATGATGGCTTTGACA 1492
Db 1409 GAATATCTATCATCAGGCTATGAAGCGTGGCGGACCTGTATGATGGCTTTGACA 1468

QY 1493 CCACCCAGTTTCATTTCGCGCTATGCGAGGTCGTACCTGCGTACACACCACTGGG 1552
Db 1469 CCACCCAGTTTCATTTCGCGCTATGCGAGGTCGTACCTGCGTACACCACTGGG 1528
QY 1553 CCGACGGAAGAGCTTGAAGCGGCTAACCTCGACTTTTGAGACCAAGCTGAGTAA 1612
Db 1529 CCGACGGAAGAGCTTGAAGCGGCTAACCTCGACTTTTGAGACCAAGCTGAGTAA 1588
QY 1613 GTAGACAGGAAAATGTCGTAATAGAGAAAGAGATTGAAGCCGGGTCGGGGTTT 1672
Db 1589 GTAGACAGGAAAATGTCGTAATAGAGAAAGAGATTGAAGCCGGGTCGGGGTTT 1648
QY 1673 ATTTCTCCGTAGATCGACACTTTATCGAACAACAGAGCCAGTTGCAAGCTGCGATC 1732
Db 1649 ATTTCTCCGTAGATCGACACTTTATCGAACAACAGAGCCAGTTGCAAGCTGCGATC 1708
QY 1733 TTCCATCGGTGTTCCACTGTGATGGAAGAGCTGTACCTGCGGTGATGATCACTGG 1792
Db 1709 TTCCATCGGTGTTCCACTGTGATGGAAGAGCTGTACCTGCGGTGATGATCACTGG 1768
QY 1793 TGAAGTCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGATCACGGAGAAA 1852
Db 1769 TGAAGTCGAAGGCTACGTAGTGAAGAAAATCACCATCAGTCCCGGATCACGGAGAAA 1828
QY 1853 CCGTGGGATACCGGCTTACACACAATAGCGAGGCTTCTTGCTATGCAAGTTACTGACA 1912
Db 1829 CCGTGGGATACCGGCTTACACACAATAGCGAGGCTTCTTGCTATGCAAGTTACTGACA 1888
QY 1913 CAGTAAAGAGAGAGCGGATCGTTCCTGTGTCAGTACATCCCGGACCAATATAGG 1972
Db 1889 CAGTAAAGAGAGAGCGGATCGTTCCTGTGTGTCAGTACATCCCGGACCAATATAGG 1948
QY 1973 ATCAGATGACTGTATATATGCGCACGAGTATATCACCCTGACGATGACAAAACTTCTGG 2032
Db 1949 ATCAGATGACTGTATATATGCGCACGAGTATATCACCCTGACGATGACAAAACTTCTGG 2008
QY 2033 TTGGGCTCAACACAGCAATTGCTCTTAAAGGTAGAGACTTAAAGAGACCAACCATGTC 2092
Db 2009 TTGGGCTCAACACAGCAATTGCTCTTAAAGGTAGAGACTTAAAGAGACCAACCATGTC 2068
QY 2093 AAAATTAACCTTTCGCGCATATAGCACAGGTTCAAGAAATGGGCTAAAGAGCGCAAG 2152
Db 2069 AAAATTAACCTTTCGCGCATATAGCACAGGTTCAAGAAATGGGCTAAAGAGCGCAAG 2128
QY 2153 ATGATCTTGATAACGAGAAAATGCTGGTACTAGAGAACGCAAGCTTACGTATGCGTCT 2212
Db 2129 ATGATCTTGATAACGAGAAAATGCTGGTACTAGAGAACGCAAGCTTACGTATGCGTCT 2188
QY 2213 TGTGGGCGTTTCGCACTAAGAAAATGATTCGTTTATGCGCCACCTGGAACGACAGCT 2272
Db 2189 TGTGGGCGTTTCGCACTAAGAAAATGATTCGTTTATGCGCCACCTGGAACGACAGCT 2248
QY 2273 GCGTAAAGTCCGAGCTCTTTTATAGCGCTTTTCCCATGTGTCGTCGTAAGACGCTCT 2332
Db 2249 GCGTAAAGTCCGAGCTCTTTTATAGCGCTTTTCCCATGTGTCGTCGTAAGACGCTCT 2308
QY 2333 TGGCCATGTGCTGAGGACAGAAAATGAAACTGGCATTCGCAACCAAGAGAGAAAAAC 2392
Db 2309 TGGCCATGTGCTGAGGACAGAAAATGAAACTGGCATTCGCAACCAAGAGAGAAAAAC 2368
QY 2393 TGTCTGACGCTCTGGAGAGAAATTAATCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAG 2452
Db 2369 TGTCTGACGCTCTGGAGAGAAATTAATCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAG 2428
QY 2453 AGGAAGCCAGAGGAGAGAGCTCCGAGAGCACTTCCACATTAATAGTGGAGCAAAAGGCA 2512
Db 2429 AGGAAGCCAGAGGAGAGAGCTCCGAGAGCACTTCCACATTAATAGTGGAGCAAAAGGCA 2488
QY 2513 TCGAGGACGCGCAGAAAGTTGTCTGCGAAGTGAAGGGCTTCAGGCGGACATCGAGCAG 2572
Db 2489 TCGAGGACGCGCAGAAAGTTGTCTGCGAAGTGAAGGGCTTCAGGCGGACATCGAGCAG 2548
QY 2573 CATTAGTTGAAACCCCGCGGTCACGTAAAGATATACCTCAAGCAAAATGACCGTATGA 2632

Db 2549 CATTAGTTGAAACCCCGCGGTCACGTAAAGTAAATACCTCAAGCAAAATGACCGTATGA 2608
QY 2633 TCGGACAGTATATCGTGTCTGCGCAAACTCTGTGTGAAAGTGCACAACTGCGACCA 2692
Db 2609 TCGGACAGTATATCGTGTCTGCGCAAACTCTGTGTGAAAGTGCACAACTGCGACCA 2668
QY 2693 CGCACCCGCTAGCAGATCAGTTAAGATCATACACACTCCGGAATATCAGAAAGTACG 2752
Db 2669 CGCACCCGCTAGCAGATCAGTTAAGATCATACACACTCCGGAATATCAGAAAGTACG 2728
QY 2753 CCGTGCACCATTCGACGCTTAAAGTCTGATGCGACAGAGAGTCCGTAACATGCGCAG 2812
Db 2729 CCGTGCACCATTCGACGCTTAAAGTCTGATGCGACAGAGAGTCCGTAACATGCGCAG 2788
QY 2813 AATTTCTAGACCTGATGAGAGCGCACGTTAGTGTACAAACGAAAGAGATTGTAAAC 2872
Db 2789 AATTTCTAGACCTGATGAGAGCGCACGTTAGTGTACAAACGAAAGAGATTGTAAAC 2848
QY 2873 GCAAACTATACACATTCGCATGATGATGCGCCGCAAGAAATCAGAAAGAGACAGTACA 2932
Db 2849 GCAAACTATACACATTCGCATGATGATGCGCCGCAAGAAATCAGAAAGAGACAGTACA 2908
QY 2933 AGGTTTCAAAAGCAGAGCTTGCAGAAAACAGATACGTGTTTGAAGTGAACAGACGTT 2992
Db 2909 AGGTTTCAAAAGCAGAGCTTGCAGAAAACAGATACGTGTTTGAAGTGAACAGACGTT 2968
QY 2993 GCGTTAAGAGAGAGAGCGTCAAGGTCTGCTCTCGGAGAACGACCAACCCCTCCCT 3052
Db 2969 GCGTTAAGAGAGAGAGCGTCAAGGTCTGCTCTCGGAGAACGACCAACCCCTCCCT 3028
QY 3053 ATCATAGGCTAGCTCTGAGAGGATCTGAAGACCCGATCCGTCGTAACAGTGCAGAA 3112
Db 3029 ATCATAGGCTAGCTCTGAGAGGATCTGAAGACCCGATCCGTCGTAACAGTGCAGAA 3088
QY 3113 CAATAGAGTGAATAGGACACCGGGGTCCGGCAAGTCACTATTTCAAGTCAACTGTCA 3172
Db 3089 CAATAGAGTGAATAGGACACCGGGGTCCGGCAAGTCACTATTTCAAGTCAACTGTCA 3148
QY 3173 CCGCACGAGATCTTGTATACAGCGGAAAGAAAATTTGTGCGCAAAATTTGAGGCCGAG 3232
Db 3149 CCGCACGAGATCTTGTATACAGCGGAAAGAAAATTTGTGCGCAAAATTTGAGGCCGAG 3208
QY 3233 TGTAAAGTGAAGGGATATGACAGATTAAGTTCGTAAGACAGTAAATTCGTTATGCTCAAG 3292
Db 3209 TGTAAAGTGAAGGGATATGACAGATTAAGTTCGTAAGACAGTAAATTCGTTATGCTCAAG 3268
QY 3293 GATGCCACAAAGCCGTGAAGTGTGTACGTTGACGAAGCTTCCGCTGCACGCGAGAG 3352
Db 3269 GATGCCACAAAGCCGTGAAGTGTGTACGTTGACGAAGCTTCCGCTGCACGCGAGAG 3328
QY 3353 CACTACTTCGCTTGAATGCTATGTCAGGCGCCGCAAGAAAGTAAATATGAGGAGAC 3412
Db 3329 CACTACTTCGCTTGAATGCTATGTCAGGCGCCGCAAGAAAGTAAATATGAGGAGAC 3388
QY 3413 CCATGCAATGCGGATTCCTTCAACATGATGCAATTAAGGTATCAATTCACCTGAAA 3472
Db 3389 CCATGCAATGCGGATTCCTTCAACATGATGCAATTAAGGTATCAATTCACCTGAAA 3448
QY 3473 AAGACATATGACCAAGACATTTCTACAGTATATCTCCCGGCTTGCACACAGCCGTTA 3532
Db 3449 AAGACATATGACCAAGACATTTCTACAGTATATCTCCCGGCTTGCACACAGCCGTTA 3508
QY 3533 CAGCTATTGATCGACACTGCTATTCGATGGAAGTGAAGAACCAAGCCGTCGAGA 3592
Db 3509 CAGCTATTGATCGACACTGCTATTCGATGGAAGTGAAGAACCAAGCCGTCGAGA 3568
QY 3593 AGAACTTGAATTCGATATTAAGGGGCCCAAGCCGAGCCAGGAGTATCATCTGA 3652
Db 3569 AGAACTTGAATTCGATATTAAGGGGCCCAAGCCGAGCCAGGAGTATCATCTGA 3628
QY 3653 CATGTTTCCGGGGGTGTTAAGCAATTGCAATGACATATCCCGGACATGAAGTATGA 3712

Db 3629 CATGTTCCGCGGGGTGAAGCAATTGCAATTCGATCCCGGACATGAACTAATGA 3688
Qy 3713 CAGCCGCGGCTCAACAAGGCTAACAGAAAAGAGTGTATGCCGTCCGGCAAAAAGTCA 3772
Db 3689 CAGCCGCGGCTCAACAAGGCTAACAGAAAAGAGTGTATGCCGTCCGGCAAAAAGTCA 3748
Qy 3773 ATGAAACCCACTGTACGCGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTG 3832
Db 3749 ATGAAACCCACTGTACGCGATCAATCAGAGCATGTGAACGTGTGCTCACCCGCACTG 3808
Qy 3833 AGGACAGGCTAGTGTGAAAACTTTCGAGGGGCGACCCATGATTAACAGCCCACTAACA 3892
Db 3809 AGGACAGGCTAGTGTGAAAACTTTCGAGGGGCGACCCATGATTAACAGCTCACTAACA 3868
Qy 3893 TACCTTAAGGAACTTTCAAGGCTACTATAGAGACTGGGAACTGAAACAAAGGAAATTA 3952
Db 3869 TACCTTAAGGAACTTTCAAGGCTACTATAGAGACTGGGAACTGAAACAAAGGAAATTA 3928
Qy 3953 TTGCTGCAATTAACAGGCCCACTCCCGTGCATTCGGTTCACTGCAAGACCAACGTTT 4012
Db 3929 TTGCTGCAATTAACAGGCCCACTCCCGTGCATTCGGTTCACTGCAAGACCAACGTTT 3988
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Db 3989 GCTGGCGAAAGCAATTGGAACCGATACTAGCCAGCGCGGTATGTACTTACCGGTTGCC 4048
Qy 4073 AGTGAAGGCACTGTCCCAAGTTTGCGGATGACAAACCACTTGGCCATTTAACGCT 4132
Db 4049 AGTGAAGGCACTGTCCCAAGTTTGCGGATGACAAACCACTTGGCCATTTAACGCT 4108
Qy 4133 TAGACGTAATTTGCAATTAAGTTTTCGCGATGAGACTTGACAAGCGGCACTGTTTCTAAC 4192
Db 4109 TAGACGTAATTTGCAATTAAGTTTTCGCGATGAGACTTGACAAGCGGCACTGTTTCTAAC 4168
Qy 4193 AGAGCATCCCACTAAGCATCCCGCGGATTAAGCGAGCGCGGTACTATTGGGACA 4252
Db 4169 AGAGCATCCCACTAAGCATCCCGCGGATTAAGCGAGCGCGGTACTATTGGGACA 4228
Qy 4253 AACACCCAGGAAACCGGAGTATGGGTACGATCAAGCATTTGCGCGGCAATCTCCCGTGA 4312
Db 4229 AACACCCAGGAAACCGGAGTATGGGTACGATCAAGCATTTGCGCGGCAATCTCCCGTGA 4288
Qy 4313 GATTTCCGCTGTTCAGCTAGCTGGGAAAGGCGACAACTGATTTGGACAGCGGAGAA 4372
Db 4289 GATTTCCGCTGTTCAGCTAGCTGGGAAAGGCGACAACTGATTTGGACAGCGGAGAA 4348
Qy 4373 CCAAGTTATCTGTGACACAGATAAAGCTGTATCCGGTGAACCGCAATCTTCTCAGCCT 4432
Db 4349 CCAAGTTATCTGTGACACAGATAAAGCTGTATCCGGTGAACCGCAATCTTCTCAGCCT 4408
Qy 4433 TAGTCCCGGAGTACAAAGAAAGCAACCCGCGCGGTCAAAAAATTTCTTGAACCAAGTTCA 4492
Db 4409 TAGTCCCGGAGTACAAAGAAAGCAACCCGCGCGGTCAAAAAATTTCTTGAACCAAGTTCA 4468
Qy 4493 AACACCACTAGTACTTGTGATCAGAGAAAAAATGAAAGTCCCGGTAAGAAATCG 4552
Db 4469 AACACCACTAGTACTTGTGATCAGAGAAAAAATGAAAGTCCCGGTAAGAAATCG 4528
Qy 4553 AATGATTCGCCCGATTTGGCATAGCGCGGTGCAAGTAAAGACTCAACCTGCTTCCGGGT 4612
Db 4529 AATGATTCGCCCGATTTGGCATAGCGCGGTGCAAGTAAAGACTCAACCTGCTTCCGGGT 4588
Qy 4613 TTCCGCGGAGGACAGGTAAGCACTGTGTTCATCAATTTGGAACCTAAATACAGAAAC 4672
Db 4589 TTCCGCGGAGGACAGGTAAGCACTGTGTTCATCAATTTGGAACCTAAATACAGAAAC 4648
Qy 4673 ACCACTTTACAGAGTGCAGAAAGCACTGCGGCACTTTAAAAACCTTTCCGCTTCCGCC 4732
Db 4649 ACCACTTTACAGAGTGCAGAAAGCACTGCGGCACTTTAAAAACCTTTCCGCTTCCGCC 4708
Qy 4733 TGAATTGTTTAACTCAGAGAGCACTCTGTGTGAAGTCTTATGCTTACCGCGCA 4792
Db 4709 TGAATTGTTTAACTCAGAGAGCACTCTGTGTGAAGTCTTATGCTTACCGCGCA 4768

Qy 4793 ACAATGAGACGTAAGTACCGCTCTTGCCAGAAAGTTGTCAAGGTGTCTGACGAGAC 4852
Db 4769 ACAATGAGACGTAAGTACCGCTCTTGCCAGAAAGTTGTCAAGGTGTCTGACGAGAC 4828
Qy 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACCACTAGACAAACGCC 4912
Db 4829 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACCACTAGACAAACGCC 4888
Qy 4913 GTAACGGCAATTCACCCCGCACATCTGAATTTGCGGATTTGCGTGTATAGGGTA 4972
Db 4889 GTAACGGCAATTCACCCCGCACATCTGAATTTGCGGATTTGCGTGTATAGGGTA 4948
Qy 4973 CAAGATGAGATTGAGCCCGCGCTCATACCGACCAAAAGGAGAAATATGCTGACT 5032
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Qy 5093 GCGGTGCATCTAATAACGTTGGCCGACAGTTTACGATTCAGACCAAGGAGACAGCA 5152
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Qy 5153 CCGCAAGATGACTGTGTGCTAGGAAAGAGTATCCAGCGCGGTGCGCTGATTTCC 5212
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Qy 5213 GAAAGCAACCAAGAGCAAGAACCTTTGAATTTCTACAAACGCTTACATGACAGTGCAG 5272
Db 5189 GAAAGCAACCAAGAGCAAGAACCTTTGAATTTCTACAAACGCTTACATGACAGTGCAG 5248
Qy 5273 ACTTAGTAATGAAATTAATCAATCAAGCTGTGCGCATTCGACTGTACTACAGGCAATT 5332
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Qy 5333 ACGAGCGGAGAAAGACCGGCTTGAATATCACTTAACCTTTGACAAACCGCTAGACA 5392
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Qy 5393 GAACTGACGCGGAGTAAACCATCTATTGCTGATTAAGAAAGTGAAGAAAGAAATCGACG 5452
Db 5369 GAACTGACGCGGAGTAAACCATCTATTGCTGATTAAGAAAGTGAAGAAAGAAATCGACG 5428
Qy 5453 CGGCACTTCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATATGAGATTCGACG 5512
Db 5429 CGGCACTTCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATATGAGATTCGACG 5488
Qy 5513 ATGAGTTAGTATGGAATTCATCCAGACAGTTGCTTGAAGGAGAAAGGATTCAGTACTA 5572
Db 5489 ATGAGTTAGTATGGAATTCATCCAGACAGTTGCTTGAAGGAGAAAGGATTCAGTACTA 5548
Qy 5573 CAAAGGAAATTTGATTTCTGACTTCGAAGGACCAAAATTCATCAAGACGCAAAAGCA 5632
Db 5549 CAAAGGAAATTTGATTTCTGACTTCGAAGGACCAAAATTCATCAAGACGCAAAAGCA 5608
Qy 5633 TGGCGAGATTAAGGCTCTGTTCCCTATATGACCAAGAAAGTAAATGAACAATGTGTGCT 5682
Db 5609 TGGCGAGATTAAGGCTCTGTTCCCTATATGACCAAGAAAGTAAATGAACAATGTGTGCT 5668
Qy 5693 ACATATTGGGTGAGACATGAGAAAGCATTCGCGGAAAGTGCCGGTGAACCATTAACCGT 5752
Db 5669 ACATATTGGGTGAGACATGAGAAAGCATTCGCGGAAAGTGCCGGTGAACCATTAACCGT 5728
Qy 5753 GGTCTAGCCGCGCCAAACGTTGCGGTGCTTTGCACTGATGACCATGACGCGCAAGAGG 5812
Db 5729 GGTCTAGCCGCGCCAAACGTTGCGGTGCTTTGCACTGATGACCATGACGCGCAAGAGG 5788
Qy 5813 TCCACAGACTTAAGAGCAATTAAGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 5872
Db 5789 TCCACAGACTTAAGAGCAATTAAGTCAAGAAAGTTACAGTATGCTCTCCACCCCTTC 5848

OY	5873	CTTAAGCAAAAAATTAAAGATGTTCAGAGAGTTCCAGTGCACGAAAGTAGTCTCTGTTTAATC	5932
Db	5849	CTTAAGCAAAAAATTAAAGATGTTCAGAGAGTTCCAGTGCACGAAAGTAGTCTCTGTTTAATC	5908
OY	5933	CGCACTACCCCGCATTTGCTTCCCGCCCGCTTAAGTACATGAAAGTGCCAGAACAGCCTACCG	5992
Db	5909	CGCACTACCCCGCATTTGCTTCCCGCCCGCTTAAGTACATGAAAGTGCCAGAACAGCCTACCG	5968
OY	5993	CTCTCTCTGCA.CA.GGGCCGAGGAGGGCCCCCGAAAGTTGTAGCGACACCGTCACATCTACAG	6052
Db	5969	CTCTCTCTGCA.CA.GGGCCGAGGAGGGCCCCCGAAAGTTGTAGCGACACCGTCACATCTACAG	6028
OY	6089	GCTCACTTTTTTCCAGCTTTAGCGGATCGGACAACTCTATTACATGATGAGACAGTTGGT	6148
Db	6029	CTGAATAACACTCCGTTGATGTCA.CA.GA.CATCTCACTGAAATAGGATTA.CAGT.GCCGA.G	6088
OY	6113	GCTCACTTTTTTCCAGCTTTAGCGGATCGGACAACTCTATTACATGATGAGACAGTTGGT	6172
Db	6173	CGTCAGACCTAGTTCACTAGAGATAGTAGACCGAAGG.CAGGTGGTGGCTGACGTTTC	6232
OY	6233	ATGCCGCTCAAAGAGCGCTCCCTCTATTCCA.CCGCCAAAGGCTAAAGAAATGCGCCGCTGG	6292
Db	6209	ATGCCGCTCAAAGAGCGCTCCCTCTATTCCA.CCGCCCAAAGGCTAAAGAAATGCGCCGCTGG	6268
OY	6293	CAGCGGGCAAAAAAGAGGCCCATCCACGCGGGCAAGAAATAGCTCTAGAGTCCCTCCACCTCT	6352
Db	6269	CAGCGGGCAAAAAAGAGGCCCATCCACGCGGGCAAGAAATAGCTCTAGAGTCCCTCCACCTCT	6328
OY	6353	CTTTTGGTGGGGTATCCATGTTCCTCGGATCAATTTTGA.CGAGAGACCGGCCCGCCAGG	6412
Db	6329	CTTTTGGTGGGGTATCCATGTTCCTCGGATCAATTTTGA.CGAGAGACCGGCCCGCCAGG	6388
OY	6413	CAGCGGTTCAAA.CCCCTGGCAACAGGCCCCCA.CGGATGTGCTTATGTCTTTCCGATGCTTTT	6472
Db	6389	CAGCGGTTCAAA.CCCCTGGCAACAGGCCCCCA.CGGATGTGCTTATGTCTTTCCGATGCTTTT	6448
OY	6473	CCGACCGGAGAAATTGATAGGCTGAGCGGCA.CAGATCACTGATCCGGAACCCGTCCTGTTTG	6532
Db	6449	CCGACCGGAGAAATTGATAGGCTGAGCGGCA.CAGATCACTGATCCGGAACCCGTCCTGTTTG	6508
OY	6533	GATCATTTGAA.CCGGGCCGAGTGA.CTCAATTAATCGTCCCGATCAG.CCGTATCTTTTC	6592
Db	6509	GATCATTTGAA.CCGGGCCGAGTGA.CTCAATTAATCGTCCCGATCAG.CCGTATCTTTTC	6568
OY	6593	CACCTACGACAGACAGACGTAGACG.CAGAGACGACGAGGACTGAATATCTGACTTAAC.CCGGGG	6652
Db	6569	CCTTACGCAACACAGACGTA.GACG.CCAAGAACAGAGGACTGAATATCTGACTTAAC.CCGGGG	6628
OY	6653	TAGGTGGGTAA.CATNTTTCGACGGA.CA.AGAGCCCTGGGGCACTTGC.AAAAGAAAGTCCGTTTC	6712
Db	6629	TAGGTGGGTAA.CATNTTTCGACGGA.CA.AGAGCCCTGGGGCACTTGC.AAAAGAAAGTCCGTTTC	6688
OY	6713	TGCAAGAACACAGCTTACAAACCGA.CCTTGAGAGCGCAATGCTCTGGAAAGAAATTCATGCCC	6772
Db	6689	TGCAAGAACACAGCTTACAAACCGA.CCTTGAGAGCGCAATGCTCTGGAAAGAAATTCATGCCC	6748
OY	6773	CGGTGCTCGACACGTCGAAAGAGAACACTCAAA.CT.CAGGTAC.CAGATGATGCCACCG	6832
Db	6749	CGGTGCTCGACACGTCGAAAGAGAACACTCAAA.CT.CAGGTAC.CAGATGATGCCACCG	6808
OY	6833	AAGCCAA.CAAAAGTATGTTTCCAGTCTCGTAAAGTATGAAATTCAGAAAGCCATAAC.CACTG	6892
Db	6809	AAGCCAA.CAAAAGTATGTTTCCAGTCTCGTAAAGTATGAAATTCAGAAAGCCATAAC.CACTG	6868
OY	6893	AGGCACTACTGTACAGACCTACGACCTGTATTA.CTCTG.CCA.CAGATCAG.CCAAAAGTCTATA	6952
Db	6869	AGGCACTACTGTACAGACCTACGACCTGTATTA.CTCTG.CCA.CAGATCAG.CCAAAAGTCTATA	6928
OY	6953	AGATCACCTTATCCGAAACCATTTGTATCTC.CAGTAGCGTACCGGCGAACTACTCCGATCAC	7012

Db	6929	AGATCACCTATCGAAACCAATGATACCAAGTAGCGTACCGGGGAATCTCCGATCAC	6998
QY	7013	AGTTCCGCTGATAGCTGTCTGTAAACAACATCTGCAATGAACTATCCGACAGTAGCATCTT	7072
Db	6989	AGTTCCGCTGATAGCTGTCTGTAAACAACATCTGCAATGAACTATCCGACAGTAGCATCTT	7048
QY	7073	ATCAGATTACTGACGAGTACGATGCTTACTTTGGATATGTAGACGAGACAGTGGCATGCC	7132
Db	7049	ATCAGATTACTGACGAGTACGATGCTTACTTTGGATATGTAGACGAGACAGTGGCATGCC	7108
QY	7133	TGGAATTACGCAACCTTGCCCGCGCTAAGCTTGAAGTTACCCGAAAAACATGAGATA	7192
Db	7109	TGGAATTACGCAACCTTGCCCGCGCTAAGCTTGAAGTTACCCGAAAAACATGAGATA	7168
QY	7193	GAGCCCCGAATATCCGAGTGCCTTTCATCAGCGATGCAAGAACACGCTCAAAATGTGC	7252
Db	7169	GAGCCCCGAATATCCGAGTGCCTTTCATCAGCGATGCAAGAACACGCTCAAAATGTGC	7228
QY	7253	TCATTTGCCGCACTAAAGAAATTTGCACGCTCAACGAGATGCGTGAATCTGCCAACACTGG	7312
Db	7229	TCATTTGCCGCACTAAAGAAATTTGCACGCTCAACGAGATGCGTGAATCTGCCAACACTGG	7288
QY	7313	ACTGAGGACATTCATATGTGGAATGCTTTTGGAAATATGCAATGTAAATGACAGTATTTGGG	7372
Db	7289	ACTGAGGACATTCATATGTGGAATGCTTTTGGAAATATGCAATGTAAATGACAGTATTTGGG	7348
QY	7373	AGGAGTTTCGCTCGGAAACCAATTAGATTACACTGAGTTTGTTCACCGCATATATGACTA	7432
Db	7349	AGGAGTTTCGCTCGGAAACCAATTAGATTACACTGAGTTTGTTCACCGCATATATGACTA	7408
QY	7433	GACTGAAAGGCCCTTAAGGCCGCGCACTAATTTGCMAAGACGTATATTTGGTCCCATTTGC	7492
Db	7409	GACTGAAAGGCCCTTAAGGCCGCGCACTAATTTGCMAAGACGTATATTTGGTCCCATTTGC	7468
QY	7493	AAGAAGTGCCTATAGATATGATTTGCTCATTGCATATGAAATGAAGACGTAAAGTTTACACAG	7552
Db	7469	AAGAAGTGCCTATAGATATGATTTGCTCATTGCATATGAAATGAAGACGTAAAGTTTACACAG	7528
QY	7553	GCACGAAACACACAGAGAAAGACCGAAATGTACAGTACATCAAGCCGCGCAAAACCCCTGG	7612
Db	7529	GCACGAAACACACAGAGAAAGACCGAAATGTACAGTACATCAAGCCGCGCAAAACCCCTGG	7588
QY	7613	CGACTGCTTACTTATGCGGAGATTCAACGGGAATTTAGTCGTAGGCTTACCGGCGCTTTGC	7672
Db	7589	CGACTGCTTACTTATGCGGAGATTCAACGGGAATTTAGTCGTAGGCTTACCGGCGCTTTGC	7648
QY	7673	TTCCAAACATTACACGCTTTTGTGACATGTTCGCGCGAGAGATTTTGTATGCAATCATAGCAG	7732
Db	7649	TTCCAAACATTACACGCTTTTGTGACATGTTCGCGCGAGAGATTTTGTATGCAATCATAGCAG	7708
QY	7733	AACACTTCAAGCAAGGAGACCCGGTATCTGGAACGGAATATCCGATCATTTGACAAAAAGCC	7792
Db	7709	AACACTTCAAGCAAGGAGACCCGGTATCTGGAACGGAATATCCGATCATTTGACAAAAAGCC	7768
QY	7769	AAGACGAAGCGTATGCGCTTAAACGCGTCTGATGATCTTTGAGAGACCTGGGTGTGGATCAAC	7828
Db	7853	CACCTACTGCACTTGATGAGTGGCGCTTTTGGAGAAATATCATCOACCATCTACCTAGCGG	7912
QY	7829	CACCTACTGCACTTGATGAGTGGCGCTTTTGGAGAAATATCATCOACCATCTACCTAGCGG	7888
Db	7913	GTACTCGTTTTAAATTTGGGGCGCATGATGAATTCGGAAATGTTCTCTACACTTTTGTGCA	7972
QY	7889	GTACTCGTTTTAAATTTGGGGCGCATGATGAATTCGGAAATGTTCTCTACACTTTTGTGCA	7948
Db	7973	ACAAGTTTTGAATGTGCTTATCGCCGACGAGAGTATCTAGAAGCGGCTTAAACGTCGA	8032
QY	7949	ACAAGTTTTGAATGTGCTTATCGCCGACGAGAGTATCTAGAAGCGGCTTAAACGTCGA	8008
Db	8033	GATGTGACGCGTTTCATTTGGCGACGACAAATCATATCATGGAGTAGTATCTTGACAAAAGAA	8092

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QY 1553 CCGACGAGAAAGTCTTGAAGCGGCTAACTCGGACTTTGACAGCAAAAGCTGTAGAG 1612
DB 1529 CCGACGAGAAAGTCTTGAAGCGGCTAACTCGGACTTTGACAGCAAAAGCTGTAGAG 1588
QY 1613 GTAGGACAGGAAATTTGCTGATTAAGAGAAAGAGATTGAAGCCCGGGTCCGGGTTT 1672
DB 1589 GTAGGACAGGAAATTTGCTGATTAAGAGAAAGAGATTGAAGCCCGGGTCCGGGTTT 1648
QY 1673 ATTTCTCCGTAGATTCACACTTTATCCAGAACACAGAGCCAGTTTCAAGCTGGATC 1732
DB 1649 ATTTCTCCGTAGATTCACACTTTATCCAGAACACAGAGCCAGTTTCAAGCTGGATC 1708
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DB 1769 TGAAGTTCGAAGGCTACGTAGTGAAGAAATCAACATCACTCCCGGATCACGGAGAAA 1828
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DB 1829 CCGTGGGATACGGGCTTACACAAATAGCGAGGCTTTGCTATGCAAAAGTTACTGACA 1888
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DB 1889 CAGTAAAGAGAGAACGGGATTCGTTCCCTGTGTGACAGTACATCCCGGACCAATATGGG 1948
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DB 2009 TTGGGCTCAACACGCAATTTGTCTTAAACGCTAGAGATTAAACAGAACCAACCACTGC 2068
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DB 2129 ATGATCTTGAATAACGAGAAATGCTGGGTACTAGAGAACGCAAGCTTACGTATGCTGCT 2188
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Db 7409 GACTGAAGGCCCTTAAGGCCGCGGCACTATTTTGCAAGAAGATTAATTTGGTCCATTCG 7468
QY 7493 AAGAATGCTATATGATTAATTCGTATGATGAGTGAAGAAAGACGTAATTTGGTCCATTCG 7552
Db 7469 AAGAATGCTATATGATTAATTCGTATGATGAGTGAAGAAAGACGTAATTTGGTCCATTCG 7528
QY 7553 GCACGAAACACACAGAGAAAGACCGAAAGTACAAAGTATCAAGCCGAGAACCCCTGG 7612
Db 7529 GCACGAAACACACAGAGAAAGACCGAAAGTATCAAGTATCAAGCCGAGAACCCCTGG 7588
QY 7613 CGACTCTTACTTATGCGGGAATTCACCGGGAATTAATGTCGTAGGCTTACCGCGCTTTC 7672
Db 7589 CGACTCTTACTTATGCGGGAATTCACCGGGAATTAATGTCGTAGGCTTACCGCGCTTTC 7648
QY 7673 TTCCAAACATTCACACGCTTTTTCGACATGTCGCGGAGGATTTTGAATGCAATCATAGCAG 7732
Db 7649 TTCCAAACATTCACACGCTTTTTCGACATGTCGCGGAGGATTTTGAATGCAATCATAGCAG 7708
QY 7733 AACACTTCAAGCAAGGCGACCCGCTACTGAGACGATATCCGATATTCGACAAAGCC 7792
Db 7709 AACACTTCAAGCAAGGCGACCCGCTACTGAGACGATATCCGATATTCGACAAAGCC 7768
QY 7793 AAGACGAGCTATGCGGTTAACCGGCTGATGATCTTGAAGACCTGGGTGTGATCAAC 7852
Db 7769 AAGACGAGCTATGCGGTTAACCGGCTGATGATCTTGAAGACCTGGGTGTGATCAAC 7828
QY 7853 CACTACTGCACTTGAATGCGATGCGCTTTGGAGAAATATCATTCACCCATCTTACCTACGG 7912
Db 7829 CACTACTGCACTTGAATGCGATGCGCTTTGGAGAAATATCATTCACCCATCTTACCTACGG 7888
QY 7913 GTACTGTTTTTAAATTCGGGGGAGATGATGAATCCGGAATGTTCCCTCAACATTTTGTCA 7972
Db 7889 GTACTGTTTTTAAATTCGGGGGAGATGATGAATCCGGAATGTTCCCTCAACATTTTGTCA 7948
QY 7973 ACAAGTTTTTGAATGCTTATGCGCAGAGATCTAGAAAGCGGCTTAAACGCTCA 8032
Db 7949 ACAAGTTTTTGAATGCTTATGCGCAGAGATCTAGAAAGCGGCTTAAACGCTCA 8008
QY 8033 GATGTCAGCCGTTCAATTGGCGACGACAACTATATCATGAGATGATTTGACAAAGAA 8092

Dh 8009 GATGTGACGCTTATTTGGCAGCAGACATCATATGAGTATCTATCTACAAAGAAA 8068
Qy 8093 TGGGTGAGAGGTGGCCGACCTGGCTCAACATGAGGTTAGATCATGACCGACGATCG 8152
Dh 8069 TGGCTGAGAGGTGGCCGACCTGGCTCAACATGAGGTTAGATCATGACCGACGATCG 8158
Qy 8153 GTGAGAGACCACTTACTTCTTGGCGGGATTTATCTTGCAGAGTTCCGTTACTTCCACAG 8212
Dh 8129 GTGAGAGACCACTTACTTCTTGGCGGGATTTATCTTGCAGAGTTCCGTTACTTCCACAG 8188
Qy 8213 CGTGCCTGGTGGGAGATCCCTGAAAAAGCGTTTAAAGTTGGGTAAACCGCTCCACAGCG 8272
Dh 8189 CGTGCCTGGTGGGAGATCCCTGAAAAAGCGTTTAAAGTTGGGTAAACCGCTCCACAGCG 8248
Qy 8273 ACGACGACGACGAGAGACAGAAAGACCGCTGCTAGATGATAAACAAGCGCTGGTTTA 8332
Dh 8249 ACGACGACGACGAGAGACAGAAAGACCGCTGCTAGATGATAAACAAGCGCTGGTTTA 8308
Qy 8333 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAAACAATA 8392
Dh 8309 GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAAACAATA 8368
Qy 8393 TTACACCTGTCTCTGCTGATGAGAACTTTGGCCAGAGAAAAAGACATTTCCAAAGCA 8452
Dh 8369 TTACACCTGTCTCTGCTGATGAGAACTTTGGCCAGAGAAAAAGACATTTCCAAAGCA 8428
Qy 8453 TCAAGAGGGAATTAAGCATCTTACAGGTGGTCCCTAAATAGTACAGATGATTTTCAT 8512
Dh 8429 TCAAGAGGGAATTAAGCATCTTACAGGTGGTCCCTAAATAGTACAGATGATTTTCAT 8488
Qy 8513 CTGACTAATTAATCAACACACCACT 8539
Dh 8489 CTGACTAATTAATCAACACCACT 8515

RESULT 7
ADL71910
ID ADL71910 standard; cDNA; 17753 BP.
XX
AC ADL71910;
XX
DT 20-MAY-2004 (first entry)
XX
DE Expression vector pCytS-OPE.
XX
KM Gene expression; vector; pCytS; ss.
XX
OS Alphavirus.
OS Human herpesvirus 4.
OS Chimeric.
XX
PN WO2004018506-A2.
XX
PD 04-MAR-2004;
XX
PF 21-AUG-2003; 2003WO-EP009291.
XX
PR 22-AUG-2002; 2002US-0404928P.
PR 11-DEC-2002; 2002US-0432259P.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY AG.
XX
PI Ivanova L, Renner WA, Saudan P;
XX
DR WPI; 2004-226795/21.
XX
PT New nucleic acid molecule comprising first, second and third
PT polynucleotide elements, useful for regulating the expression of a
PT polypeptide or an untranslated RNA molecule.
XX
PS Example 2; SEQ ID NO 22; 112bp; English.
XX
CC The present sequence is that of expression vector pCytS-OPE. A claimed

CC nucleic acid molecule comprises: (A) a first polynucleotide element which
CC encodes an RNA molecule comprising (a) at least one cis-acting sequence
CC element, (b) a first nucleotide sequence comprising a first open reading
CC frame, the first open reading frame having a nucleotide sequence encoding
CC an RNA-dependent RNA polymerase, and (c) at least one second nucleotide
CC sequence comprising (i) a second open reading frame (S1) encoding a
CC polypeptide, (ii) a nucleotide sequence complementary to all or a part of
CC the second open reading frame (S1) and (iii) a nucleotide sequence
CC encoding an untranslated RNA molecule or its complement, where the second
CC nucleotide sequence is operably linked to a promoter which is recognised
CC by the RNA-dependent RNA polymerase; (B) a second polynucleotide element
CC comprising an origin of replication; and (C) a third polynucleotide
CC element encoding a replication initiation factor capable of recognising
CC the origin of replication. The nucleic acid molecule, expression systems
CC and vector systems of the invention allow the production of polypeptides
CC and untranslated RNA molecules in host cells. In a specific embodiment,
CC the invention includes the combination of a herpesvirus mini-replicon
CC unit, e.g. the cis-acting replication origin oriP and replication
CC initiation factor EBNA1 from Epstein Barr virus, with pCytS ADL71889,
CC creating pCytS-OPE. Due to the presence of OriP and EBNA1, the novel
CC vector is maintained episomally in the form of several DNA copies in cell
CC nuclei. These multiple DNA copies may be transcribed from a Rous sarcoma
CC virus or cytomegalovirus promoter into pCytS RNA replicons, but remain
CC inactive unless cells are shifted to a certain temperature. Only after
CC temperature induction does replicon replication occur, followed by RNA
CC accumulation and translation in the cell cytoplasm, and production of the
CC polypeptide of interest.

SO Sequence 17753 BP; 4502 A; 4902 C; 4209 G; 4140 T; 0 U; 0 Other;
Query Match 89.7%; Score 7657.2; DB 12; Length 17753;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7642; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 893 ATTGACGGCTGATGACACATCTATTGAATCAAAAGCCGACCAATTGCACTACATCAAA 952
Dh 869 ATTGACGGCTGATGACACATCTATTGAATCAAAAGCCGACCAATTGCACTACATCAAA 928
Qy 953 TGGAGAAAGCGATGTAAGCTAGAGTACGAGCCGAGAGTCCGTTTGTGTGCAACTGC 1012
Dh 929 TGGAGAAAGCGATGTAAGCTAGAGTACGAGCCGAGAGTCCGTTTGTGTGCAACTGC 988
Qy 1013 AAAAAGCTTCCCGCAATTTGAGGTAGTACGACGACGAGTCACTCAATGACCATGTCTA 1072
Dh 989 AAAAAGCTTCCCGCAATTTGAGGTAGTACGACGACGAGTCACTCAATGACCATGTCTA 1048
Qy 1073 ATGCCAAGACATTTTCCGATTTGCCCACTGTAATCTAATGAGCTGAGAGTTCTTACCAAG 1132
Dh 1049 ATGCCAAGACATTTTCCGATTTGCCCACTGTAATCTAATGAGCTGAGAGTTCTTACCAAG 1108
Qy 1133 CGAGATCTTGGACATGAGGCGACCGGCTGTGTAAGTTTTCGAGACACAGATTC 1192
Dh 1109 CGAGATCTTGGACATGAGGCGACCGGCTGTGTAAGTTTTCGAGACACAGATTC 1168
Qy 1193 ATTGTCTGCCCCCATCGTATGTCAGAAAGACCCGACCGCATGATGAATATCCAGTA 1252
Dh 1169 ATTGTCTGCCCCCATCGTATGTCAGAAAGACCCGACCGCATGATGAATATCCAGTA 1228
Qy 1253 AACTGGCGGAAAAAGCGTGCAGATTTCAAAACAAGAACTTGATGAGAAAGTTAAGATC 1312
Dh 1229 AACTGGCGGAAAAAGCGTGCAGATTTCAAAACAAGAACTTGATGAGAAAGTTAAGATC 1288
Qy 1313 TCCGGACCGTATCTGATACGCGCGGATCTGAAACACATGCTCTGCTTTCACAAACAATG 1372
Dh 1289 TCCGGACCGTATCTGATACGCGCGGATCTGAAACACATGCTCTGCTTTCACAAACAATG 1348
Qy 1373 TTACTCTCAACATCGTGCAGATTTCCGTCATGACGAGACGATGATATCAACCTCCCG 1432
Dh 1349 TTACTCTCAACATCGTGCAGATTTCCGTCATGACGAGACGATGATATCAACCTCCCG 1408
Qy 1433 GAACTATCTATCATCAGGCTATGAAAGCGGTGCGGACCTGTACTGATGATGGCTTCGACA 1492
Dh 1409 GAACTATCTATCATCAGGCTATGAAAGCGGTGCGGACCTGTACTGATGATGGCTTCGACA 1468

QY 1493 CCACCCAGTTTCATGTTCTCCGCTATGCGAGGTTGTAACCTTGGCTACCAACCAACTGGG 1552
DB 1469 CCACCCAGTTTCATGTTCTCCGCTATGCGAGGTTGTAACCTTGGCTACCAACCAACTGGG 1528
QY 1553 CCACCCAGTTTCATGTTCTCCGCTATGCGAGGTTGTAACCTTGGCTACCAACCAACTGGG 1612
DB 1529 CCACCCAGTTTCATGTTCTCCGCTATGCGAGGTTGTAACCTTGGCTACCAACCAACTGGG 1588
QY 1613 GTAGGACAGGAAATGTCATATGAGAAAGAGGTTGAAAGCCGGGTCCGGGTTT 1672
DB 1589 GTAGGACAGGAAATGTCATATGAGAAAGAGGTTGAAAGCCGGGTCCGGGTTT 1648
QY 1673 ATTTCTCCGATGATGCACTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1732
DB 1649 ATTTCTCCGATGATGCACTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1708
QY 1733 TTCCATCCGATGATGCACTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1792
DB 1709 TTCCATCCGATGATGCACTTATCCAGAACACAGAGCCAGCTTGCAGAGCTGGCATC 1768
QY 1793 TGAGTTCGAGAGGCTACGATGTAAGAAATACCATCAGTCCCGGAGTACCGGAGAAA 1852
DB 1769 TGAGTTCGAGAGGCTACGATGTAAGAAATACCATCAGTCCCGGAGTACCGGAGAAA 1828
QY 1853 CCGTGGGATACCGGCTTACACAAATAGCGAGGCTTCTTGCTATGCAAAAGTTTACTGCA 1912
DB 1829 CCGTGGGATACCGGCTTACACAAATAGCGAGGCTTCTTGCTATGCAAAAGTTTACTGCA 1888
QY 1913 CAGTAAAGAGAAACGGGATTCGTTCCCTGTGTGACATGTCACGTCACCAATATGCG 1972
DB 1889 CAGTAAAGAGAAACGGGATTCGTTCCCTGTGTGACATGTCACGTCACCAATATGCG 1948
QY 1973 ATCAGATGATGATGTAATGAGCCAGGATATATCAGCTGACGATGACCAAAATCTTGG 2032
DB 1949 ATCAGATGATGATGTAATGAGCCAGGATATATCAGCTGACGATGACCAAAATCTTGG 2008
QY 2033 TTGGGCTCAACACAGCGAATTTGTCTTAAACGTAAGACTTAAACAGAACCAACCACTGC 2092
DB 2009 TTGGGCTCAACACAGCGAATTTGTCTTAAACGTAAGACTTAAACAGAACCAACCACTGC 2068
QY 2093 AAAATTACCTTTCGCGATCATAGACACAGGCTTACCAAAATGGGCTTAAAGAGCGCAAG 2152
DB 2069 AAAATTACCTTTCGCGATCATAGACACAGGCTTACCAAAATGGGCTTAAAGAGCGCAAG 2128
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DB 2129 ATGATCTGTAATGAGAAATGCTGGTACTAGAGAACGCAAGCTTACGATAGGCTGCT 2188
QY 2213 TGTGGCGTTTCGCACTAAGAAATGATTCGTTTATGCGCCACCTGAAACGCAAGCT 2272
DB 2189 TGTGGCGTTTCGCACTAAGAAATGATTCGTTTATGCGCCACCTGAAACGCAAGCT 2248
QY 2273 GCGTAAAGTCCAGCCTCTTTTAAAGCGCTTTCCCATGTGCTCGTATGAGACGCTCTT 2332
DB 2249 GCGTAAAGTCCAGCCTCTTTTAAAGCGCTTTCCCATGTGCTCGTATGAGACGCTCTT 2308
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DB 2309 TGCCCATGTGCTGAGGACAGAAATTTGAACTGGCATTTGCAACCAAAAGAGGAAATAC 2268
QY 2393 TGTGCAAGTCTCGAGGAAATTAATCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAGG 2452
DB 2369 TGTGCAAGTCTCGAGGAAATTAATCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAGG 2428
QY 2453 AGGAAACCAAGAGCGAGAAAGTCCGAGAGACATTTCCACATTAATGAGGCAAAAGGCA 2512
DB 2429 AGGAAACCAAGAGCGAGAAAGTCCGAGAGACATTTCCACATTAATGAGGCAAAAGGCA 2488
QY 2513 TCAGAGGAGCGGAGAGTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATTCGAGACAG 2572
DB 2489 TCAGAGGAGCGGAGAGTGTCTGCGAAGTGGAGGGGCTCCAGGCGGACATTCGAGACAG 2548

QY 2573 CATTAAGTAAACCCCGCGGCTACGTAAGATTAATCTCTCAAGCAATGACCGTATGA 2632
DB 2549 CATTAAGTAAACCCCGCGGCTACGTAAGATTAATCTCTCAAGCAATGACCGTATGA 2608
QY 2633 TCGGACAGTATATCGTGTCTGGCCAACTCTGTGTGTAAGAAATGCAAACTGCAACAG 2692
DB 2609 TCGGACAGTATATCGTGTCTGGCCAACTCTGTGTGTAAGAAATGCAAACTGCAACAG 2568
QY 2693 CGCACCCGCTAGCAGATCAGGTTAAGATCATACACTCCGGAATCAGGAAGTACG 2752
DB 2669 CGCACCCGCTAGCAGATCAGGTTAAGATCATACACTCCGGAATCAGGAAGTACG 2728
QY 2753 CGGTGCAACATTCGACGCTTAAAGTACTAGTGCACAGAGAGTGTGCTGATGCGCAG 2812
DB 2729 CGGTGCAACATTCGACGCTTAAAGTACTAGTGCACAGAGAGTGTGCTGATGCGCAG 2788
QY 2813 AATTCTGACACTGATGAGAGGCGCACGTTAGTGTGTAACAGGAAGAGTGTGTGAC 2872
DB 2789 AATTCTGACACTGATGAGAGGCGCACGTTAGTGTGTAACAGGAAGAGTGTGTGAC 2848
QY 2873 GCNAACCTATACACATTTGCATGATGAGCCCGCCCAAGAAATACAGAAAGAGCAGTACA 2932
DB 2849 GCNAACCTATACACATTTGCATGATGAGCCCGCCCAAGAAATACAGAAAGAGCAGTACA 2908
QY 2933 AGGTTCAAAAGCAGAGCTTGCAGAAAACAGATACGTTTGAAGCTGTGACAGAAAGCTT 2992
DB 2909 AGGTTCAAAAGCAGAGCTTGCAGAAAACAGATACGTTTGAAGCTGTGACAGAAAGCTT 2868
QY 2993 GCGTTAAGAAAGAGAGGCTCAGGCTGCTGCTCCGGAAGAACTGACCAACCTCCCT 3052
DB 2969 GCGTTAAGAAAGAGAGGCTCAGGCTGCTGCTCCGGAAGAACTGACCAACCTCCCT 3028
QY 3053 ATCATAGGCTAGCTCTGAGAGGACTGAAAGACCCGACCTGCGGTCCGTAACAGGTCGAAA 3112
DB 3029 ATCATAGGCTAGCTCTGAGAGGACTGAAAGACCCGACCTGCGGTCCGTAACAGGTCGAAA 3088
QY 3113 CAATAGAGTATAGGACACACCGGGGTCCGGCAGTACGATTAATCAAGTCACTGTCA 3172
DB 3089 CAATAGAGTATAGGACACACCGGGGTCCGGCAGTACGATTAATCAAGTCACTGTCA 3148
QY 3173 CCGCACAGATCTTGTTCACAGCGGAAAGAAATTTGTCGCAATTTGAGAGCGAG 3232
DB 3149 CCGCACAGATCTTGTTCACAGCGGAAAGAAATTTGTCGCAATTTGAGAGCGAG 3208
QY 3233 TGTAAAGTGAAGGGTATGACAGATTAAGTGAAGACAGTAAATTCGTTATCTCAACG 3292
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QY 3293 GATGCCAACAAAGCCGTAGAAATGCTGTAAGTGAAGAGCTTCCGCTGCAACGAGAG 3352
DB 3269 GATGCCAACAAAGCCGTAGAAATGCTGTAAGTGAAGAGCTTCCGCTGCAACGAGAG 3328
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QY 3413 CCATGCAATGCGGATTTCTCAACATGATGCACTTAAAGGTAATTTCAATCACTGAAA 3472
DB 3389 CCATGCAATGCGGATTTCTCAACATGATGCACTTAAAGGTAATTTCAATCACTGAAA 3448
QY 3473 AAGACATATGACCAAGACATTTCTAAGATTAATCTCCCGGCTGCAACAGCAGTTA 3532
DB 3449 AAGACATATGACCAAGACATTTCTAAGATTAATCTCCCGGCTGCAACAGCAGTTA 3508
QY 3533 CAGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3592
DB 3509 CAGCTATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3568
QY 3593 AGAACAATTGAATTCGATTAACAGGGGCAACAAGCCGAAGCCAGGGGATATCATCTGCA 3652
DB 3569 AGAACAATTGAATTCGATTAACAGGGGCAACAAGCCGAAGCCAGGGGATATCATCTGCA 3628
QY 3653 CATGTTCCGCGGGTGAAGCAATTCGCAATTCGATTCGCGGACATGAAATGTAATGA 3712

Db 3629 CATGTTTCCGGGGTGGGTTAAAGCAATTGCAAAATCGACTATCCGGGACATGAATAATATGA 3688
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Db 3749 ATGAAAACCCATGTATCGCGATCAATCAGAGATGTGAAGGTGTCTCAACCGCATG 3808
Qy 3833 AGGACAGGCTATGTGTGAAAACTTTGCAAGGGCGAACCATGGATTAAAGACCCCATACA 3882
Db 3809 AGGACAGGCTATGTGTGAAAACTTTGCAAGGGCGAACCATGGATTAAAGCTCATACA 3868
Qy 3893 TACCTAAAGGAACTTTCAAGGCTACTATAGAGACTGGGAAAGTGAACACAAAGGAAATTA 3952
Db 3869 TACCTAAAGGAACTTTCAAGGCTACTATAGAGACTGGGAAAGTGAACACAAAGGAAATTA 3928
Qy 3953 TTGCTGCAATTAACAGCCCACTCCCGTGCMAATCCGTTCAAGTGCMAAGACAAAGTTT 4012
Db 3929 TTGCTGCAATTAACAGCCCACTCCCGTGCMAATCCGTTCAAGTGCMAAGACAAAGTTT 3988
Qy 4013 GCTGGGCGAAAGCATTTGGAACCGGATCTAGGCAAGCGCGGTATGTACTTAACGGTTGCC 4072
Db 3989 GCTGGGCGAAAGCATTTGGAACCGGATCTAGGCAAGCGCGGTATGTACTTAACGGTTGCC 4048
Qy 4073 AGTGGAGCGAATCTGTTCCACAGTTTGCGAGTGAACAAACCAATTCGGCCATTTAAAGCCT 4132
Db 4049 AGTGGAGCGAATCTGTTCCACAGTTTGCGAGTGAACAAACCAATTCGGCCATTTAAAGCCT 4108
Qy 4133 TAGACGTAATTTGCAATTAAGTTTTCGCGCATGAGCTTGACAAAGCGGACTGTTTTCTAAAC 4192
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Qy 4193 AGAGCATCCCACTAAGCTATCCGCGCATTAAGCGAGGCGCGTACTATGGAGCA 4252
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Db 4529 AATGATTCGCGCGATTTGCACTAGCCGCTGAGTAAGAACTACCACTGCGCTTTCGCGGT 4588
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QY 5933 CGCACTATCCCGCATTTGTTCCCGCCCGTAAGTACATAGAAAGTCCGAAACAGCTTACCG 5992
DB CGCACTATCCCGCATTTGTTCCCGCCCGTAAGTACATAGAAAGTCCGAAACAGCTTACCG 5968
QY 5993 CTCCTCTGACAGCGCGAGAGAGGCCCGCGAAGTTAGCGACACCGTCACTACATCTACAG 6052
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QY 6053 CTGATTAACACTCGCTGATGATGTCACAGACATCTCACTGATATGATGATGACAGTAGCGAAG 6112
DB CTGATTAACACTCGCTGATGATGTCACAGACATCTCACTGATATGATGATGACAGTAGCGAAG 6088
QY 6113 GCTCACCTTTTTCGAGCTTTAGCGGATCGGACACTATTAATTAAGTATGACAGTGTGT 6172
DB GCTCACCTTTTTCGAGCTTTAGCGGATCGGACACTATTAATTAAGTATGACAGTGTGT 6148
QY 6173 CGTCAGAGACTAGTCTACTAGATAGTAGACCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGT 6232
DB CGTCAGAGACTAGTCTACTAGATAGTAGACCGAGAGAGTGTGTGTGTGTGTGTGTGTGTGT 6208
QY 6233 ATGCGCTCAAGAGCTGCGCTCTATTCACCGCCAGGCTTAAAGAGATGAGCGCTGTG 6292
DB ATGCGCTCAAGAGCTGCGCTCTATTCACCGCCAGGCTTAAAGAGATGAGCGCGCTGTG 6268
QY 6293 CAGCGCGAAGAAAGAGCCCACTCCACCGGAGCATTAAGTATGATGATGATGATGATGATGAT 6352
DB CAGCGCGAAGAAAGAGCCCACTCCACCGGAGCATTAAGTATGATGATGATGATGATGATGAT 6328
QY 6353 CTTTGTGTGGGTATCCATGTCCTCGGATCAATTTTGAAGAGAGAGCGCGCGCAGG 6412
DB CTTTGTGTGGGTATCCATGTCCTCGGATCAATTTTGAAGAGAGAGCGCGCGCAGG 6388
QY 6413 CAGCGGTACAAACCCCTGGCAACAGGCCCAAGATGTCCTATGCTTTTGGATCGTTT 6472
DB CAGCGGTACAAACCCCTGGCAACAGGCCCAAGATGTCCTATGCTTTTGGATCGTTT 6448
QY 6473 CCGAGCGAGATTTAGAGCTGAGCGGAGAGAGTGAATGATGATGATGATGATGATGATGAT 6532
DB CCGAGCGAGATTTAGAGCTGAGCGGAGAGAGTGAATGATGATGATGATGATGATGATGAT 6508
QY 6533 GATCATTTGAACCGGCGGAGAGTGAATCAATTAATGTCCTCGATCAGCGGTATCTTTT 6592
DB GATCATTTGAACCGGCGGAGAGTGAATCAATTAATGTCCTCGATCAGCGGTATCTTTT 6568
QY 6593 CACTACGCAAGCAGAGAGTGAAGCAGAGAGAGAGAGTGAATCAATCACTAAACCGG 6652
DB CACTACGCAAGCAGAGAGTGAAGCAGAGAGAGAGAGTGAATCAATCACTAAACCGG 6628
QY 6653 TAGTGCGGTATATTTTCGACGAGACAGAGCCCTGGGCACTTGCAAAAGAGCGTTC 6712
DB TAGTGCGGTATATTTTCGACGAGACAGAGCCCTGGGCACTTGCAAAAGAGCGTTC 6688
QY 6713 TGCAGAACAGCTTACAGAACCGACCTTGAAGCGCAATGTCCTGAAGAAATTCATGCC 6772
DB TGCAGAACAGCTTACAGAACCGACCTTGAAGCGCAATGTCCTGAAGAAATTCATGCC 6748
QY 6773 CGGTGCTCGACAGTGCAGAAAGAGAGCACTCAACTCAGGTACAGATGATGCCACCG 6832
DB CGGTGCTCGACAGTGCAGAAAGAGAGCACTCAACTCAGGTACAGATGATGCCACCG 6808
QY 6833 AAGCAACAAGAGGTACAGGTCTGTAAGAGAAATCAGAAAGCATTAACCATG 6892
DB AAGCAACAAGAGGTACAGGTCTGTAAGAGAAATCAGAAAGCATTAACCATG 6868
QY 6893 AGGAGTACTGTGAGAGTACAGTGTATTAATCTGACAGATCAGCCAGAAATGCTATA 6952
DB AGGAGTACTGTGAGAGTACAGTGTATTAATCTGACAGATCAGCCAGAAATGCTATA 6928

QY 6953 AGATCACTATCCGAAACCATTTGTAATCCAGTATGCGTACCGCGAACTACTCCGATCCAC 7012
DB AGATCACTATCCGAAACCATTTGTAATCCAGTATGCGTACCGCGAACTACTCCGATCCAC 6988
QY 7013 AGTTGCTGAGT 7072
DB AGTTGCTGAGT 7048
QY 7073 ATCAGATTAATCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7132
DB ATCAGATTAATCGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7108
QY 7133 TGGATATCGCAACTTCTGCTCCCGCTTAAGTTAGAAATTAATCCGAAATTAATGATATA 7192
DB TGGATATCGCAACTTCTGCTCCCGCTTAAGTTAGAAATTAATCCGAAATTAATGATATA 7168
QY 7193 GAGCCCGAATATCCGACAGT 7252
DB GAGCCCGAATATCCGACAGT 7228
QY 7253 TCATTCGCGCACTAAAGAAATTTGCAAGTCAAGAGATGCGTGAATGCGCAACTGG 7312
DB TCATTCGCGCACTAAAGAAATTTGCAAGTCAAGAGATGCGTGAATGCGCAACTGG 7288
QY 7229 TCATTCGCGCACTAAAGAAATTTGCAAGTCAAGAGATGCGTGAATGCGCAACTGG 7288
DB TCATTCGCGCACTAAAGAAATTTGCAAGTCAAGAGATGCGTGAATGCGCAACTGG 7264
QY 7313 ACTCAGGACATTCATGTCGAAATGCTTGGAAATATGATGATGATGATGATGATGATGATGAT 7372
DB ACTCAGGACATTCATGTCGAAATGCTTGGAAATATGATGATGATGATGATGATGATGATGAT 7348
QY 7373 AGGAGTTGCTGGGAGAGCAATTAAGATTAACATGATGATGATGATGATGATGATGATGAT 7432
DB AGGAGTTGCTGGGAGAGCAATTAAGATTAACATGATGATGATGATGATGATGATGATGAT 7408
QY 7433 GACTGAAAGCCCTTAAGGCGCGCGCACTTTTGCAAAGACGTATAATTTGTGCCATTCG 7492
DB GACTGAAAGCCCTTAAGGCGCGCGCACTTTTGCAAAGACGTATAATTTGTGCCATTCG 7468
QY 7409 GACTGAAAGCCCTTAAGGCGCGCGCACTTTTGCAAAGACGTATAATTTGTGCCATTCG 7468
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QY 7493 AAGAAGTGCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7552
DB AAGAAGTGCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7528
QY 7469 AAGAAGTGCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7528
DB AAGAAGTGCCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7504
QY 7553 GCACGAAACACACAGAAAGAGCCGAAAGTCAATGATGATGATGATGATGATGATGATGATGAT 7612
DB GCACGAAACACACAGAAAGAGCCGAAAGTCAATGATGATGATGATGATGATGATGATGATGAT 7588
QY 7529 GACGAAACACACAGAAAGAGCCGAAAGTCAATGATGATGATGATGATGATGATGATGATGAT 7588
DB GACGAAACACACAGAAAGAGCCGAAAGTCAATGATGATGATGATGATGATGATGATGATGAT 7564
QY 7613 CGACTGCTTACTTATGCGGAGATTCACCGGAAATTAAGTGTGATGATGATGATGATGATGAT 7672
DB CGACTGCTTACTTATGCGGAGATTCACCGGAAATTAAGTGTGATGATGATGATGATGATGAT 7648
QY 7589 CGACTGCTTACTTATGCGGAGATTCACCGGAAATTAAGTGTGATGATGATGATGATGATGAT 7648
DB CGACTGCTTACTTATGCGGAGATTCACCGGAAATTAAGTGTGATGATGATGATGATGATGAT 7624
QY 7673 TTCCAAACATTCACAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 7732
DB TTCCAAACATTCACAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 7708
QY 7649 TTCCAAACATTCACAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 7708
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QY 7733 AACACTTCAAGCAAGGCGACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 7792
DB AACACTTCAAGCAAGGCGACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 7768
QY 7709 AACACTTCAAGCAAGGCGACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 7768
DB AACACTTCAAGCAAGGCGACCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 7744
QY 7793 AAGACGACGCTATGCGGTTAACCGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 7852
DB AAGACGACGCTATGCGGTTAACCGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 7828
QY 7769 AAGACGACGCTATGCGGTTAACCGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 7828
DB AAGACGACGCTATGCGGTTAACCGGTCTGATGATGATGATGATGATGATGATGATGATGATGAT 7804
QY 7853 CACTACTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7912
DB CACTACTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7888
QY 7829 CACTACTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7888
DB CACTACTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7864
QY 7913 GATGCTGCTTTTAAATTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7972
DB GATGCTGCTTTTAAATTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7948
QY 7889 GATGCTGCTTTTAAATTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7948
DB GATGCTGCTTTTAAATTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 7924
QY 7973 ACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8032
DB ACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8008
QY 7949 ACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8008
DB ACACAGTTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8008
QY 8033 GATGCTGCTTTTAAATTCGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 8092

Db 8009 GATGTGAGGGTTCATTGGGAGACACATCATATGAGTATGATCTGACAAAGAAA 8068
Qy 8093 TGCTGAGAGGTGGCCACCTGGCTCAACATGAGGTTAAGATCATGACGACATCTGC 8152
Db 8069 TGGCTGAGAGGTGGCCACCTGGCTCAACATGAGGTTAAGATCATGACGACATCTGC 8128
Qy 8153 GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGCGTTACCTTCA 8212
Db 8129 GTGAGAGACCACTTACTTCTGCGCGGATTTATCTTGCAAGATTGCGTTACCTTCA 8188
Qy 8213 CGTGGCCCGTGGCGGATTCCTTGAAAAGCTGTTAAGTTGGTAAACCGTCCACCG 8272
Db 8189 CGTGGCCCGTGGCGGATTCCTTGAAAAGCTGTTAAGTTGGTAAACCGTCCACCG 8248
Qy 8273 ACGAGAGACCAAGAGACGAGACGCGCTGTAGATGAAACAAAGCGTGGTTA 8332
Db 8249 ACGAGAGACCAAGAGACGAGACGCGCTGTAGATGAAACAAAGCGTGGTTA 8308
Qy 8333 GAGTAGGTATTAACAGGACCTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACA 8392
Db 8309 GAGTAGGTATTAACAGGACCTTTAGCAGTGGCCGTGACGACCCGGTATGAGGTAGACA 8368
Qy 8393 TTACACCTGTCTTCTGCGCATTTGAACTTTGCCGAGCAAAAGACATTTCCAGCCA 8452
Db 8369 TTACACCTGTCTTCTGCGCATTTGAACTTTGCCGAGCAAAAGACATTTCCAGCCA 8428
Qy 8453 TCGAGAGGGAATTAAGACATCTACAGTGGTCTTAATAGTACAGATAGACATTTTCA 8512
Db 8429 TCGAGAGGGAATTAAGACATCTTACGTTGCTTAAATAGTACAGATAGACATTTTCA 8488
Qy 8513 CTGACTAATATCTACACACCAACCACT 8539
Db 8489 CTGACTAATATCTACACACCAACCACT 8515

RESULT 8
AAK77354
ID AAK77354 standard; DNA; 9951 BP.

AAK77354;

09-AUG-1999 (first entry)

DE Polynucleotide sequence of pSinpRep 5.

KW Nucleic acid identification; exogenous protein; gene sorting;
growth factor; membrane receptor; Sindbis virus; ss.

OS Synthetic.

PN WO9925876-A1.

PD 27-MAY-1999.

PF 17-NOV-1998; 98WO-US024520.

PR 17-NOV-1997; 97US-00972218.

PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.

PI Bailey JE, Renner WA, Orberger GH, Koller D;

DR WPI; 1999-357620/30.

PT Isolating genes encoding proteins with selected properties, useful for
identifying therapeutic agents or targets.

PS Disclosure; Fig 11A-C; 136pp; English.

CC The invention relates to the identification of a recombinant nucleic acid
encoding an exogenous protein having a selected property. The method
comprises preparing a population of eukaryotic host cells, culturing the

CC cells under suitable conditions and identifying cells that contain the
CC recombinant nucleic acid. The method is used to sort genes according to
CC the type of proteins they express, and also to identify new ligand/
CC receptor interactions. Typical applications of the nucleic acid and the
CC exogenous protein are in isolation of new growth factors, cytokines,
CC membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
CC which may be useful as therapeutic agents or therapeutic targets, e.g.
CC apoptosis-promoting or tumour suppressing proteins, regulators of cell
CC proliferation or metabolic processes etc. The protein can also be used to
CC screen for specific modulators. The nucleic acid can also be used as
CC sources of therapeutic antisense or ribozyme sequences. The method allows
CC the protein (rather than a partial DNA sequence) to be isolated and,
CC since a wide range of cells can be used, they can be expressed with the
CC correct glycosylation pattern

SO Sequence 9951 BP; 2852 A; 2461 C; 2464 G; 2174 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 2; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 893 ATTGACGCGGTAGTACACATTTGATGATCAACAGCCGACCAATTGGACTACATCAAA 952
Db 1 ATTGACGCGGTAGTACACATTTGATGATCAACAGCCGACCAATTGGACTACATCAAA 60
Qy 953 TGGAGAGCCAGTATGTAACGTAGACGTAGACCCCGAGTCCGTTGTCTGCACTGC 1012
Db 61 TGGAGAGCCAGTATGTAACGTAGACGTAGACCCCGAGTCCGTTGTCTGCACTGC 120
Qy 1013 AAAAAAGCTTCCCGCAATTTGAGTATGACAGAGGTCTCTCCAAATGACCATGTA 1072
Db 121 AAAAAAGCTTCCCGCAATTTGAGTATGACAGAGGTCTCTCCAAATGACCATGTA 180
Qy 1073 ATGCGAGAGCAATTTGCGCATCTGGCAGTAACTATCGAGCTGAGAGTTCTTACCAAG 1132
Db 181 ATGCGAGAGCAATTTGCGCATCTGGCAGTAACTATCGAGCTGAGAGTTCTTACCAAG 240
Qy 1133 CGAGCATCTTGCACATAGGAGCGACGCGCTCTGATAGATGTTTCCGAGCAGCAGATC 1192
Db 241 CGAGCATCTTGCACATAGGAGCGACGCGCTCTGATAGATGTTTCCGAGCAGCAGATC 300
Qy 1193 ATTGTGTCTGCCCATGCGTATGTCAGAGAACCCGACCGCATATGAAATAGCCAGTA 1252
Db 301 ATTGTGTCTGCCCATGCGTATGTCAGAGAACCCGACCGCATATGAAATAGCCAGTA 360
Qy 1253 AACTGGGGGAAAAAGCCGTGCAAGTTTCAACAGAACTTGATGAGAGATTAAGATC 1312
Db 361 AACTGGGGGAAAAAGCCGTGCAAGTTTCAACAGAACTTGATGAGAGATTAAGATC 420
Qy 1313 TCCGGAACCTTCTGATACGCGGATGCTGAAACACCATGCTCTGTTTCAACAGATC 1372
Db 421 TCCGGAACCTTCTGATACGCGGATGCTGAAACACCATGCTCTGTTTCAACAGATC 480
Qy 1373 TTACTTGCACATGCGTGCAGATATTTCCGTATGACAGAGCTGTATATCAACGCTCCG 1432
Db 481 TTACTTGCACATGCGTGCAGATATTTCCGTATGACAGAGCTGTATATCAACGCTCCG 540
Qy 1433 GAATATCTATCATCAGGCTATGAAAGCGCGGACCCGTACTGATGGCTTCCACA 1492
Db 541 GAATATCTATCATCAGGCTATGAAAGCGCGGACCCGTACTGATGGCTTCCACA 600
Qy 1493 CCACCCAGTTGATGTTCTCGGCTATGAGCAGGTTGTGTAACCTGCTACACCAACTGGG 1552
Db 601 CCACCCAGTTGATGTTCTCGGCTATGAGCAGGTTGTGTAACCTGCTACACCAACTGGG 660
Qy 1553 CCGAGAGAAAGTCTTGAAGCGCGTAAATCATGCACTTTGACAGCAAAAGCTGAGTAA 1612
Db 661 CCGAGAGAAAGTCTTGAAGCGCGTAAATCATGCACTTTGACAGCAAAAGCTGAGTAA 720
Qy 1613 GTAGAGACAGAAATTTGCGATATGAGAGAAAGAGTTGAACCCGCGGTGCGGGATT 1672
Db 721 GTAGAGACAGAAATTTGCGATATGAGAGAAAGAGTTGAACCCGCGGTGCGGGATT 780

QY 1673 ATTTCTCCGTAGAGTCGACACTTTATCCAGAACACAGAGCCAGCTTGCAAGAGCTGGCATC 1732
DB 781 ATTTCTCCGTAGAGTCGACACTTTATCCAGAACACAGAGCCAGCTTGCAAGAGCTGGCATC 840
QY 1733 TTCCATCGGTGTTTCCACTTGAATGGAAGCAGTGTGTAACCTGGCCGTGTGATCACTGG 1792
DB 841 TTCCATCGGTGTTTCCACTTGAATGGAAGCAGTGTGTAACCTGGCCGTGTGATCACTGG 900
QY 1793 TGAATTGCGAAGGCTACGTAGTGAAGAAATCACCATCAGTCCCGGAGTCAACGGAGAAA 1852
DB 901 TGAATTGCGAAGGCTACGTAGTGAAGAAATCACCATCAGTCCCGGAGTCAACGGAGAAA 960
QY 1853 CCGTGGGATACGGCGTTACACACATAAGCGGGCTTCTTGTAATGCAAAAGTTACTGACA 1912
DB 961 CCGTGGGATACGGCGTTACACACATAAGCGGGCTTCTTGTAATGCAAAAGTTACTGACA 1020
QY 1913 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTGACGTACATCCCGGCCACCATATGCG 1972
DB 1021 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTGACGTACATCCCGGCCACCATATGCG 1080
QY 1973 ATCAGATGACTGTATATATGAGCCACGATATATCAGTGAAGTGAACAAAACTTCTGG 2032
DB 1081 ATCAGATGACTGTATATATGAGCCACGATATATCAGTGAAGTGAACAAAACTTCTGG 1140
QY 2033 TTGGGCTCAACCAAGCAATTTGTCTTAAACGTAGACTTAACAGGAACCAACCACTGC 2092
DB 1141 TTGGGCTCAACCAAGCAATTTGTCTTAAACGTAGACTTAACAGGAACCAACCACTGC 1200
QY 2093 AAAATTAACCTTTCGCGATCAGACACAGAGGTTACAGCAATGGGCTTAAGAGGCGCAAG 2152
DB 1201 AAAATTAACCTTTCGCGATCAGACACAGAGGTTACAGCAATGGGCTTAAGAGGCGCAAG 1260
QY 2153 ATGATCTTGTATACGAGAAAAATGCTGGGTACTAGAGAACCAAGCTTACGTATGGCTGT 2212
DB 1261 ATGATCTTGTATACGAGAAAAATGCTGGGTACTAGAGAACCAAGCTTACGTATGGCTGT 1320
QY 2213 TGTGGGGGTTTTCGCACTTAAGAAATACATTGCTTTATCGCCCACTGGAACCGACACT 2272
DB 1321 TGTGGGGGTTTTCGCACTTAAGAAATACATTGCTTTATCGCCCACTGGAACCGACACT 1380
QY 2273 GCGTAAAGTCCAGCCTCTTTTACGCTTTTCCCATGTGCTGCTGCTGCTGCTGCTGCT 2332
DB 1381 GCGTAAAGTCCAGCCTCTTTTACGCTTTTCCCATGTGCTGCTGCTGCTGCTGCTGCT 1440
QY 2333 TGCCCATGTGCTGAGGCGAGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 2392
DB 1441 TGCCCATGTGCTGAGGCGAGAAATGGAATGGAATGGAATGGAATGGAATGGAATGGA 1500
QY 2393 TGCCTGCAAGTCTCGGAGGAATTAATCATGAGGCGCAAGGCTGCTTTGAGAGTGTCAAG 2452
DB 1501 TGCCTGCAAGTCTCGGAGGAATTAATCATGAGGCGCAAGGCTGCTTTGAGAGTGTCAAG 1560
QY 2453 AGGAAGCAGAGCGGAGAGCTCCGAGAGCACTTCCACCATTAATGAGGAGCAAAAGGCA 2512
DB 1561 AGGAAGCAGAGCGGAGAGCTCCGAGAGCACTTCCACCATTAATGAGGAGCAAAAGGCA 1620
QY 2513 TCGAGGAGCGGAGAGGTTGTCTGCGAATGGAAGGCTCCAGGCGGACATCGAGCAG 2572
DB 1621 TCGAGGAGCGGAGAGGTTGTCTGCGAATGGAAGGCTCCAGGCGGACATCGAGCAG 1680
QY 2573 CATTAGTGAAGAACCCCGCGGCTCACTGAAGATTAATCTCAAGCAAAAGCACTGATGA 2632
DB 1681 CATTAGTGAAGAACCCCGCGGCTCACTGAAGATTAATCTCAAGCAAAAGCACTGATGA 1740
QY 2633 TCGGACGATATATGTTGTCTGCGCAAACTGTGCTGAGAGATGCCAACTGGCACAG 2692
DB 1741 TCGGACGATATATGTTGTCTGCGCAAACTGTGCTGAGAGATGCCAACTGGCACAG 1800
QY 2693 CGGACCCGCTAGAGATCAGGTTAAGATCATTAACAACCTCGGAGAGTCAAGAGGATACG 2752
DB 1801 CGGACCCGCTAGAGATCAGGTTAAGATCATTAACAACCTCGGAGAGTCAAGAGGATACG 1860
QY 2753 CGGTCGAACCATAGACGCTTAAAGTACTGATGCCAGAGAGGTGCCGTACATGGCCAG 2812

DB 1861 CGGTCGAACCATAGACGCTTAAAGTACTGATGCCAGAGAGGTGCCGTACATGGCCAG 1920
QY 2813 AATTTCTAGACACTGAGTGAAGGCGCCAGCTTAATGTATACAAAGAAAGATTTGTGAAC 2872
DB 1921 AATTTCTAGACACTGAGTGAAGGCGCCAGCTTAATGTATACAAAGAAAGATTTGTGAAC 1980
QY 2873 GCAAACTATACCATTTCCATGATGATGCCCGCCCAAGAAATACAGAGAGAGCACTACA 2932
DB 1981 GCAAACTATACCATTTCCATGATGATGCCCGCCCAAGAAATACAGAGAGAGCACTACA 2040
QY 2933 AGGTTACAAAGAGAGCTTGAAGAAACAGAGTACGTGTTTGAACGTGAACAAAGGTT 2992
DB 2041 AGGTTACAAAGAGAGCTTGAAGAAACAGAGTACGTGTTTGAACGTGAACAAAGGTT 2100
QY 2993 GCGTTAAGAGAGAGGCTCAGTCTGTGCTCTCGGAGAACTGACCAACCTCCT 3052
DB 2101 GCGTTAAGAGAGAGGCTCAGTCTGTGCTCTCGGAGAACTGACCAACCTCCT 2160
QY 3053 ATCATGAGCTAGCTTGAAGGACTGAAGACCCGACCTGCGGTCCCGTACAGAGTCGAAA 3112
DB 2161 ATCATGAGCTAGCTTGAAGGACTGAAGACCCGACCTGCGGTCCCGTACAGAGTCGAAA 2220
QY 3113 CAATAGAGTGAATAGGCAACCGGGGTCCGGCAAGTCACTATTAATCAATCTGTCA 3172
DB 2221 CAATAGAGTGAATAGGCAACCGGGGTCCGGCAAGTCACTATTAATCAATCTGTCA 2280
QY 3173 CGGACGAGATCTTGTACACGCGGAAAGAAATTTGTCCGAAATTTGAGGCGGACG 3232
DB 2281 CGGACGAGATCTTGTACACGCGGAAAGAAATTTGTCCGAAATTTGAGGCGGACG 2240
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QY 3293 GATGCCAAGAGCCGTAGAGAGTGTAGCTTGAACGAACGTTCCGGTCCAGAGGAG 3352
DB 2401 GATGCCAAGAGCCGTAGAGAGTGTAGCTTGAACGAACGTTCCGGTCCAGAGGAG 2460
QY 3353 CACTACTTCGCTTGAATGCTATGCTCAGGCCCCGCAAGAGGATTAATGCGGAGACC 3412
DB 2461 CACTACTTCGCTTGAATGCTATGCTCAGGCCCCGCAAGAGGATTAATGCGGAGACC 2520
QY 3413 CCATGCAATGCGGATCTTCAACATGATGCAATTAAGGTCATTTCAATCACTGAAA 3472
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QY 3473 AAGACATATGACCAAGACATTTCAAGTATATCTCCCGGCTTGCACACAGCCGTTA 3532
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QY 3533 CAGCTATTGATGACACTGCAATTAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAG 3592
DB 2641 CAGCTATTGATGACACTGCAATTAAGTGAAGAAAGTGAAGAAAGTGAAGAAAGTGAAG 2700
QY 3593 AGAACATTGAATTCATATTAACAGGGGCAACAAAGCCGAAGCCAGGGGATATCATCTGA 3652
DB 2701 AGAACATTGAATTCATATTAACAGGGGCAACAAAGCCGAAGCCAGGGGATATCATCTGA 2760
QY 3653 CATGTTTCCGGGGGTGAGTGAAGCAATTTGCAATTCATATCCCGGACATGAAGTAAATGA 3712
DB 2761 CATGTTTCCGGGGGTGAGTGAAGCAATTTGCAATTCATATCCCGGACATGAAGTAAATGA 2820
QY 3713 CAGCGCGGCTCACAAAGGGCTTAACGAGAAAGAGATGATGCGTCCGCAAAAGTCA 3772
DB 2821 CAGCGCGGCTCACAAAGGGCTTAACGAGAAAGAGATGATGCGTCCGCAAAAGTCA 2880
QY 3773 ATGAAAAACCACTGTACGAGATCAGATCAGAGCATGTGAACGTGTTCTCACCCGCACTG 3832
DB 2881 ATGAAAAACCACTGTACGAGATCAGATCAGAGCATGTGAACGTGTTCTCACCCGCACTG 2940
QY 3833 AGGACAGGCTAGTGTGAAAACCTTGCAGGGGCAACCATGATTAAGCAAGCCCATTAACA 3892

Db 2941 AGCAGCGCTAGTGTGAAAACTTGCAGGCGACCCATGATTAAGACGCCCACTAAC
Qy 3893 TACCTAAAGAACTTTCAAGGCTACTATAGAGACTGGGAAGCTGAACACAAAGGAATTA 3952
Db 3001 TACTTAAGAACTTTCAAGGCTACTATAGAGACTGGGAAGCTGAACACAAAGGAATTA 3060
Qy 3953 TTGCTGCAATTAACAGCCCCCACTCCCGTGCATTCGGTTCAGTGCAGACCAACGTTT 4012
Db 3061 TTGCTGCAATTAACAGCCCCCACTCCCGTGCATTCGGTTCAGTGCAGACCAACGTTT 3120
Qy 4013 GCTGGGGAAGAACTTGAACCCGATCTAGACGAGCGCGATATGTTACTTACCGTTGCC 4072
Db 3121 GCTGGGGAAGAACTTGAACCCGATCTAGACGAGCGCGATATGTTACTTACCGTTGCC 3180
Qy 4073 AGTGAAGCAACTTTCCACAGTTTGGGATGACAAACCATTCGGCCATTACGCT 4132
Db 3181 AGTGAAGCAACTTTCCACAGTTTGGGATGACAAACCATTCGGCCATTACGCT 3240
Qy 4133 TAGACGTAATTTGCATTAAATTTTTCGCGATGACTTGAACAGCGGACTGTTTTCTAAC 4192
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Qy 4193 AGAGCATCCCACTAACGTAACATCCCGCGATTAAGGAGCGCGTATGTTGGACA 4252
Db 3301 AGAGCATCCCACTAACGTAACATCCCGCGATTAAGGAGCGCGTATGTTGGACA 3360
Qy 4253 ACAGCCGAGGAACCCGCAAGTATGGGTACGATCAAGCATTCGCGCGAATCTCCGCTA 4312
Db 3361 ACAGCCGAGGAACCCGCAAGTATGGGTACGATCAAGCATTCGCGCGAATCTCCGCTA 3420
Qy 4313 GATTTCCGCTGTTCCAGCTAGCTGGGAAGGACACAACTTGAATTTGCAGACGGGAGAA 4372
Db 3421 GATTTCCGCTGTTCCAGCTAGCTGGGAAGGACACAACTTGAATTTGCAGACGGGAGAA 3480
Qy 4373 CCAGATTAATCTCTGCACAGATTAACCTGTCCTCGGTGAACCGCAATCTCTCAACGCT 4432
Db 3481 CCAGATTAATCTCTGCACAGATTAACCTGTCCTCGGTGAACCGCAATCTCTCAACGCT 3540
Qy 4433 TAGTCCCGAGTACAAAGAGAAAGCAACCCGCGCGTCAAAAAATTTCTGAACCAAGTTCA 4492
Db 3541 TAGTCCCGAGTACAAAGAGAAAGCAACCCGCGCGTCAAAAAATTTCTGAACCAAGTTCA 3600
Qy 4493 AACACCACTAGTACTTGTGTATCAAGAGAAAAATTTGAAGTCCCGGTAAAGAAATCG 4552
Db 3601 AACACCACTAGTACTTGTGTATCAAGAGAAAAATTTGAAGTCCCGGTAAAGAAATCG 3660
Qy 4553 AATGATCGCCCGATTTGGCATAGCCGGTGCAGTAAGAACTAACCTGCTTTCCGGT 4612
Db 3661 AATGATCGCCCGATTTGGCATAGCCGGTGCAGTAAGAACTAACCTGCTTTCCGGT 3720
Qy 4613 TTCCGCGGAGGCAACGGTACGACTGTGTATCAATTTGAACCTTAATACGAAGAAC 4672
Db 3721 TTCCGCGGAGGCAACGGTACGACTGTGTATCAATTTGAACCTTAATACGAAGAAC 3780
Qy 4673 ACCACTTTACAGCACTGGGAAGACCATGCGGCACTTTAAAAACCTTTCCGCTTCGCGCC 4732
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Qy 4733 TGAATTTGTTAACTCAGAGAGCAACCTCTGTGTGAAGTCTTAATGCTACGCGACCGCA 4792
Db 3841 TGAATTTGTTAACTCAGAGAGCAACCTCTGTGTGAAGTCTTAATGCTACGCGACCGCA 3900
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Db 3901 ACAGTGAAGCACTAGTACACCGCTCTTGCAGAAAGTTGTTCAGAGGTGTCTGCACCGAGAC 3960
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Db 4021 GTACACGGCAATTCACCCCGACCATCTGAATTCGTGATTCGTTCGTGTATGAGGTA 4080

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Dh 4501 GAACTGACGCGAGCTTAACCATCTATTGCTGATTAAGAAATGAGAAAGAAATGACG 4560
Qy 5453 CGGCACTTCCAACTTAAGAGTCTGTAAACAAGCTGAAAGATTAAGATATGAGATTCGACG 5512
Dh 4561 CGGCACTTCCAACTTAAGAGTCTGTAAACAAGCTGAAAGATTAAGATATGAGATTCGACG 4620
Qy 5513 ATGAGTTAGTATGATTCATCCAGACAGTTGCTTGAAGGAGAAAGAAAGAAATTCAGTACTA 5572
Dh 4621 ATGAGTTAGTATGATTCATCCAGACAGTTGCTTGAAGGAGAAAGAAAGAAATTCAGTACTA 4680
Qy 5573 CAAGAGAAATTTGATATTCGTAATTCGAAAGCAACAAATTCATCAAGCAAGCAAAAGACA 5632
Dh 4681 CAAGAGAAATTTGATATTCGTAATTCGAAAGCAACAAATTCATCAAGCAAGCAAAAGACA 4740
Qy 5633 TGCGGAGATTAAGTCTGTTCCCTTATATGACAGAAAGTATGAACAATGTGTGCT 5692
Dh 4741 TGCGGAGATTAAGTCTGTTCCCTTATATGACAGAAAGTATGAACAATGTGTGCT 4800
Qy 5693 AATATTTGGGTGAGACATGGAAGCAATCCGCGAAAGTGGCGGTGACCATTAACCGT 5752
Dh 4801 AATATTTGGGTGAGACATGGAAGCAATCCGCGAAAGTGGCGGTGACCATTAACCGT 4860
Qy 5753 CGTCTAGCCCGCCCAAAACGTTGCGCTTTCATGATGACATGACGCAAGAAAGG 5812
Dh 4861 CGTCTAGCCCGCCCAAAACGTTGCGCTTTCATGATGACATGACGCAAGAAAGG 4920
Qy 5813 TCACAGACTTGAAGCAATTAACGTAAGAAAGTTACAGTATGCTCTCAACCCCTTC 5872
Dh 4921 TCACAGACTTGAAGCAATTAACGTAAGAAAGTTACAGTATGCTCTCAACCCCTTC 4980
Qy 5873 CTAAGCAAAATTAAGAAATTTGAAGGTTCAAGTTCAGTACGAAAGTATGCTCTGTTAATC 5932
Dh 4981 CTAAGCAAAATTAAGAAATTTGAAGGTTCAAGTTCAGTACGAAAGTATGCTCTGTTAATC 5040
Qy 5933 CGCACACTCCCGCAATTCGTTCCCGCGCTTAAGTACATGAAGTCCAGAAAGCTTACCG 5992
Dh 5041 CGCACACTCCCGCAATTCGTTCCCGCGCTTAAGTACATGAAGTCCAGAAAGCTTACCG 5100
Qy 5993 CTCTCTCTGCAACAGCCGAGAGGCGCCGAAAGTTTGAAGCAACGCTCACATCTACG 6052
Dh 5101 CTCTCTCTGCAACAGCCGAGAGGCGCCGAAAGTTTGAAGCAACGCTCACATCTACG 5160
Qy 6053 CTGATTAACCTCGCTTGAATGTACAGACATCTCACTGATATGATGAGAGTACGAG 6112
Dh 5161 CTGATTAACCTCGCTTGAATGTACAGACATCTCACTGATATGATGAGAGTACGAG 5220

QY 6113 GCTCACTTTTTCGAGCTTTAGCGGATCGAACAACCTCTATTACTAGTATGACAGTTGGT 6172
Db 5221 GCTCACTTTTTCGAGCTTTAGCGGATCGAACAACCTCTATTACTAGTATGACAGTTGGT 5280
QY 6173 CGTCAGGACCTAGTTCACTAGAGTAGTACAGCGAAGGACAGTGTGTGGTCTGACCTTC 6232
Db 5281 CGTCAGGACCTAGTTCACTAGAGTAGTACAGCGAAGGACAGTGTGTGGTCTGACCTTC 5340
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Db 5341 ATGCGCTCAAGAGCTGCCCCCTATTCTCACCGCCAGGCTTAAAGAAATGAGCCCGCTGG 5400
QY 6293 CAGCGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTGTGAGTCCCTCCACTCT 6352
Db 5401 CAGCGCAAGAAAAGAGCCCACTCCACCGGCAAGCAATAGCTGTGAGTCCCTCCACTCT 5460
QY 6353 CTTTGGTGGGGTATCCATGTCCTCGGATCAATTTTCGACGAGAACGGCCCGCCAGG 6412
Db 5461 CTTTGGTGGGGTATCCATGTCCTCGGATCAATTTTCGACGAGAACGGCCCGCCAGG 5520
QY 6413 CAGCGGTACAACCCCTGGCAACAGGCCCCACGAGTGTGCTATGTCTTTGCGATCGTTT 6472
Db 5521 CAGCGGTACAACCCCTGGCAACAGGCCCCACGAGTGTGCTATGTCTTTGCGATCGTTT 5580
QY 6473 CCGACGAGAGATTGATGAGCTGAGCCGCAAGATTACTGATGCCAACCCGTCCTGTTG 6532
Db 5581 CCGACGAGAGATTGATGAGCTGAGCCGCAAGATTACTGATGCCAACCCGTCCTGTTG 5640
QY 6533 GATCATTTTGAACCGGGGAGAGTGAACCTATTAATATGTCCTCCATTCAGCCGATCTTTT 6592
Db 5641 GATCATTTTGAACCGGGGAGAGTGAACCTATTAATATGTCCTCCATTCAGCCGATCTTTT 5700
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Db 5701 CACTACCGAAG 5760
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Db 5821 TGGAGAACGAGCTTACGAAACCGACCTTGAAGGCAATGTCTGGAAGAAATTCATGCCC 5880
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Db 5941 AAGCCAAACAAAGTAGTACCAGTCTCTGTAAAGTAAAGAAATCAGAAAGCAATAACA 6900
QY 6893 AGGACACTAGTACGAGCTACGACTGTATACTCTGACAGATCAGCCGAGATGCTATA 6952
Db 6001 AGGACACTAGTACGAGCTACGACTGTATACTCTGACAGATCAGCCGAGATGCTATA 6960
QY 6953 AGATCACTATCCGAAACCAATTTACTCCAGTAGCGTACCGGCAATCTCCGATCCAC 7012
Db 6061 AGATCACTATCCGAAACCAATTTACTCCAGTAGCGTACCGGCAATCTCCGATCCAC 6120
QY 7013 AGTTGCTGTAGCTGTGTAAACAATATCTGATGAGAACTATCCGACAGTAGCACTT 7072
Db 6121 AGTTGCTGTAGCTGTGTAAACAATATCTGATGAGAACTATCCGACAGTAGCACTT 6180
QY 7073 ATCAGATTACTGACGAGTAGTACGATGCTTGTGATAGTAGAGACGAGTAGTGGC 7132
Db 6181 ATCAGATTACTGACGAGTAGTACGATGCTTGTGATAGTAGAGACGAGTAGTGGC 6240
QY 7133 TGGATACTGCAACCTTCTGCCCGGCTAAGCTTAAAGTAAACCCGAAAACATAGAGATA 7192
Db 6241 TGGATACTGCAACCTTCTGCCCGGCTAAGCTTAAAGTAAACCCGAAAACATAGAGATA 6300
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Db 6301 GAGCCCCGAATATCCGAGTAGTGGGTTCCATCAGCAGTAGAGAACAGCTTCAAAAATGTGC 6360
QY 7253 TCAATGCCGAACCTAAAGAAATTTGCAAGTCAAGAGATGCGTGAACCTGCCAACCTGG 7312
Db 6361 TCAATGCCGAACCTAAAGAAATTTGCAAGTCAAGAGATGCGTGAACCTGCCAACCTGG 6420
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Db 6421 ACTCAGCGACATTCATCAATGTGCAATGTCTTTCGAAAATATGATGATTAAGACGATATTTGG 6480
QY 7373 AGGAGTTGCTGCGAAGCCCAATTAGATTAACCTAGATTGTTCACCGCATATGATGCTA 7432
Db 6481 AGGAGTTGCTGCGAAGCCCAATTAGATTAACCTAGATTGTTCACCGCATATGATGCTA 6540
QY 7433 GACTGAAGGCCCTTAAGGCGCGGCACTATTTTCGAAAAGCGTAAATTTGGTCCCATTCG 7492
Db 6541 GACTGAAGGCCCTTAAGGCGCGGCACTATTTTCGAAAAGCGTAAATTTGGTCCCATTCG 6600
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Db 6601 AAGAAAGTGCCTATGATAGATTGCTCATGAGACATGAAAAGAGACGTGAAGTTACACAG 6660
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Db 6841 AACACTTCAAGCAAGGCGACCCGCTACTGGAACCGAATATCCGATCATTCGACAAAAGCC 6900
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Db 6901 AAGACGAGCTATGAGGCTTAAACCGGTCTGATGATCTTGGAGGACCTGGGCTGATCAAC 6960
QY 7853 CACTACTCGACTTGAATGAGTGGCGCTTTCGAGAAATATCATCAACCACTTACCTACG 7912
Db 6961 CACTACTCGACTTGAATGAGTGGCGCTTTCGAGAAATATCATCAACCACTTACCTACG 7020
QY 7913 GTTACTGTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCACACTTTTGTCA 7972
Db 7021 GTTACTGTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTCACACTTTTGTCA 7080
QY 7973 ACAAGTTTGAATGTCGTTATTCGACGAGAGATCTAGAAAGCGGCTTAAACGTC 8032
Db 7081 ACAAGTTTGAATGTCGTTATTCGACGAGAGATCTAGAAAGCGGCTTAAACGTC 7140
QY 8033 GATGTCAGCGCTTCAATTTGCGAGCAACACATCATCATGAGAGTATCTGACMAAGAA 8092
Db 7141 GATGTCAGCGCTTCAATTTGCGAGCAACACATCATCATGAGAGTATCTGACMAAGAA 7200
QY 8093 TGGCTAGAGAGTTCGCGCACTGCTCAACATGAGAGTTAAAGTATCGACAGCATG 8152
Db 7201 TGGCTAGAGAGTTCGCGCACTGCTCAACATGAGAGTTAAAGTATCGACAGCATG 7260
QY 8153 GTGAGAGACACCTTACTCTGCGGGGAGTTATATCTGCAAGATGAGTTACTTCCACAG 8212
Db 7261 GTGAGAGACACCTTACTCTGCGGGGAGTTATATCTGCAAGATGAGTTACTTCCACAG 7320
QY 8213 CGTCCGCGTGGCGGATCCCTGAAAAGCTGTTTAAGTTGGTAAACCGCTCCACGCG 8272
Db 7321 CGTCCGCGTGGCGGATCCCTGAAAAGCTGTTTAAGTTGGTAAACCGCTCCACGCG 7380
QY 8273 ACGACGAGCAAGCAAGAACAGAGACGCGCTCTGCTAATGATGAACAAAGGCGTGGTTA 8332

Db	7281	ACGACGACCAAGACGAAACAGAAAGCCGCTCTGCTAGATGAAACAAAGGCGTGGTTTA	7442
Qy	8333	GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCCGTACACACCCGGTATAGTAGACAAATA	8352
Db	7441	GAGTAGGTATTAACAGGCACTTTAGCAGTGGCCCGTACACACCCGGTATAGTAGACAAATA	7500
Qy	8393	TTACACCTGCTCTACTGGCATTTTGGCCACAGCAAAAGACATTTCCAAAGCA	8452
Db	7501	TTACACCTGCTCTACTGGCATTTTGGCCACAGCAAAAGACATTTCCAAAGCA	7566
Qy	8453	TCAGAGGGGAATTAAGCATCTCTACGCTGTGCTCTAAATAGTCAGCATATGATTTTCAT	8512
Db	7561	TCAGAGGGGAATTAAGCATCTCTACGCTGTGCTCTAAATAGTCAGCATATGATTTTCAT	7620
Qy	8513	CTGACTAATTAACACACACACACCTT	8539
Db	7621	CTGACTAATTAACACACACACACCTT	7647
RESULT 10			
ID	AAD04742	AAD04742 standard; DNA; 9951 BP.	
AC	AAD04742;		
XX	17-JUL-2001 (first entry)		
DE	Alphaviral vector psINrep5 DNA.		
XX	psINrep5; alphaviral vector; vaccine; therapy; cancer; antiparasitic;		
KW	antimicrobial; anticancer; anti-HIV; antiviral; infectious disease;		
KW	Human immunodeficiency virus; HIV; influenza; passive immunisation;		
KW	carcinoma; liver; skin; stomach; ovarian tumour; ds.		
XX	Synthetic.		
OS	WO200130989-A2.		
FN	03-MAY-2001.		
PD	26-OCT-2000; 2000WO-IB001557.		
XX	27-OCT-1999; 99US-0161796P.		
XX	(CYTO-) CYTOS BIOTECHNOLOGY AG.		
PA	(RENN/) RENNEN W A.		
PA	(NIEB/) NIEBA L.		
XX	Renner WA, Nieba L;		
F1	WPI; 2001-306631/32.		
XX	Preparing alphaviral vectors with mutations in a selected gene, for use		
PT	as vaccines, particularly against pathogens that mutate rapidly,		
PT	comprises replicating in the presence of a nucleoside analog.		
XX	Claim 4; Fig 4; 103pp; English.		
XX	The present invention relates to a method for preparing viral vectors		
CC	which comprises inserting a gene of interest into an alphaviral vector		
CC	such as pyrites, psINrep5 and replicating the vector in the presence of		
CC	an alphaviral replicase and nucleoside analogues (5'-azacytidine (AZT), FU-		
CC	5', fluorouridine) to produce a modified gene of interest. The replication		
CC	is repeated until the modified gene in 90 % of the vector population		
CC	contains a mutation in the modified gene which is 90-99 % identical with		
CC	the gene of interest. The vector populations are used in vaccines for		
CC	treatment or prevention of a wide variety of infectious diseases (viral		
CC	or parasitic, e.g. human immuno deficiency virus (HIV), influenza,		
CC	Trypanosoma or Plasmodium) and cancers such as liver carcinoma, stomach		
CC	carcinoma, skin carcinoma and ovarian tumours. Vaccines containing the		
CC	mutant populations will therefore be effective against viral escape		
CC	mutants. Multigenic cell ensures that expressed proteins		
CC	are correctly glycosylated. Antisera raised against the vaccines can be		

[illegible]

Db 901 TGGATTGCGAAGGCTACGTAGTAAGAAATCAACATCACTCCCGGATCACCGAGAAA 960
Qy 1853 CCGTGGGATACGGGTTACACAAATAGCAGGGCTTCTGTATGCAAAAGTTACTGACA 1912
Db 961 CCGTGGGATACGGGTTACACAAATAGCAGGGCTTCTGTATGCAAAAGTTACTGACA 1020
Qy 1913 CAGTAAAGGAGAACGGGTAATGTTCCCTGTGTGACGTACATCCGGCCACCATATGCG 1972
Db 1021 CAGTAAAGGAGAACGGGTAATGTTCCCTGTGTGACGTACATCCGGCCACCATATGCG 1080
Qy 1973 ATCAGATGATGGTATATATGCGCACGGAATATATCACTGTGACCAAAAATTCTGTG 2032
Db 1081 ATCAGATGATGGTATATATGCGCACGGAATATATCACTGTGACCAAAAATTCTGTG 1140
Qy 2033 TTGGGCTCAACACGCGAATTGTCAATTAACGCTAGCACTAACAGAAACCAACCATG 2092
Db 1141 TTGGGCTCAACACGCGAATTGTCAATTAACGCTAGCACTAACAGAAACCAACCATG 1200
Qy 2093 AAAATTACCTTCTGCGCATATAGCACAGGTTCAAGCAATGGGCTAAGAGCGCAAG 2152
Db 1201 AAAATTACCTTCTGCGCATATAGCACAGGTTCAAGCAATGGGCTAAGAGCGCAAG 1260
Qy 2153 ATGATCTTGATTAACGAGAAATGCTGGGTACTAGAGAACCAAGCTTAGCTATGCTGCT 2212
Db 1261 ATGATCTTGATTAACGAGAAATGCTGGGTACTAGAGAACCAAGCTTAGCTATGCTGCT 1320
Qy 2213 TGTGGGGCTTTCGACACTAAGAAAGTACATCGTTTATGCGCCACCTGGAACGACAGCT 2272
Db 1321 TGTGGGGCTTTCGACACTAAGAAAGTACATCGTTTATGCGCCACCTGGAACGACAGCT 1380
Qy 2273 GCGTAAAGTCCAGCCTCTTTTAGCGCTTTTCCATGCTGCTAGTGAAGCACTCTT 2332
Db 1381 GCGTAAAGTCCAGCCTCTTTTAGCGCTTTTCCATGCTGCTAGTGAAGCACTCTT 1440
Qy 2333 TGGCCATGTGCTGAGGCAAGAAATGGAATCTGGCATTTGCAACCAAGAGAGAAAAC 2392
Db 1441 TGGCCATGTGCTGAGGCAAGAAATGGAATCTGGCATTTGCAACCAAGAGAGAAAAC 1500
Qy 2393 TGGTGAAGTCTGAGGAGAAATTTAGTCAATGAGGCAAGGCTGTTTGAAGATGCTCAG 2452
Db 1501 TGGTGAAGTCTGAGGAGAAATTTAGTCAATGAGGCAAGGCTGTTTGAAGATGCTCAG 1560
Qy 2453 AGGAAGCAGAGCGAGAAAGCTCCGAGAACACTTCCACATTAGTGGCAGACAAAGGCA 2512
Db 1561 AGGAAGCAGAGCGAGAAAGCTCCGAGAACACTTCCACATTAGTGGCAGACAAAGGCA 1620
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Db 1621 TCGAGGCAAGCGGCAAGATTTGTCTGCGAAGTGAAGGGCTTCAGGCGGACATCGAGCAG 1680
Qy 2573 CATTAGTTGAAACCCCGCGGCTCAGTAAAGATTAATCACTCAAGCAAAATGACCGTATGA 2632
Db 1681 CATTAGTTGAAACCCCGCGGCTCAGTAAAGATTAATCACTCAAGCAAAATGACCGTATGA 1740
Qy 2633 TCGGACAGTATATGTTGTCTGCGCAAACTGTGTGAAGAAATGCCAAACTGCAACAG 2692
Db 1741 TCGGACAGTATATGTTGTCTGCGCAAACTGTGTGAAGAAATGCCAAACTGCAACAG 1800
Qy 2693 CGGACCCGCTAGCAGATCAGGTTAAGATCAATACACTCCGGAAGATCAGGAAGTATCG 2752
Db 1801 CGGACCCGCTAGCAGATCAGGTTAAGATCAATACACTCCGGAAGATCAGGAAGTATCG 1860
Qy 2753 CGGTCGAACATTCGAGGCTAAGTACTGATGCGAGAGAGAGGCGCTGCAATGGCAG 2812
Db 1861 CGGTCGAACATTCGAGGCTAAGTACTGATGCGAGAGAGAGGCGCTGCAATGGCAG 1920
Qy 2813 AATTCTAGCACTGAGTGAAGGCGCACTTAGTGTACAAGAAAGAGATTTGTGAACC 2872
Db 1921 AATTCTAGCACTGAGTGAAGGCGCACTTAGTGTACAAGAAAGAGATTTGTGAACC 1980
Qy 2873 GCAAACTATACCAATTGCGATGATGGCCCGCAAGAAATACAGAAAGAGACATGACA 2932

Db 1981 GCAAACTATACCAATTGCGATGATGCGCCCGCCCAAGAAATACAGAAAGAGACATGACA 2040
Qy 2933 AGGTTACAAAGCAGAGCTTGGCAGAAACAGAGTACCTGTTTGAAGTGAACAAGCGTT 2992
Db 2041 AGGTTACAAAGCAGAGCTTGGCAGAAACAGAGTACCTGTTTGAAGTGAACAAGCGTT 2100
Qy 2993 GCGTTAAGAAAGAGAGCTTCAAGTCTGCTCTTCGAGAGACTGACCAACCTCTCCT 3052
Db 2101 GCGTTAAGAAAGAGAGAGCTTCAAGTCTGCTCTTCGAGAGACTGACCAACCTCTCCT 2160
Qy 3053 ATCATAGCTAGTCTGAGAGGACTGAGAACCCGACCTCGGCTCCGTCACAAAGTGSAA 3112
Db 2161 ATCATAGCTAGTCTGAGAGGACTGAGAACCCGACCTCGGCTCCGTCACAAAGTGSAA 2220
Qy 3113 CATATAGTATGATAGCAGACACCGGGTCCGGCAAGTCACTATATTAAGTCAACTGTCA 3172
Db 2221 CATATAGTATGATAGCAGACACCGGGTCCGGCAAGTCACTATATTAAGTCAACTGTCA 2280
Qy 3173 CGGACAGATCTTGTACAGCGGAAAGAAATTTGTCGCAAAATTTAGAGCGGACG 3232
Db 2281 CGGACAGATCTTGTACAGCGGAAAGAAATTTGTCGCAAAATTTAGAGCGGACG 2340
Qy 3233 TGTATAGCTGAGGGGTATGCAAGTACGTCGAGACAGTATGCTTATGCTCAAG 3292
Db 2341 TGTATAGCTGAGGGGTATGCAAGTACGTCGAGACAGTATGCTTATGCTCAAG 2400
Qy 3293 GATGCCAAGAGCGGTAGAGTGTGTAGCTTGAAGCAAGAGCTTCCGTCGACGACAGAG 3352
Db 2401 GATGCCAAGAGCGGTAGAGTGTGTAGCTTGAAGCAAGAGCTTCCGTCGACGACAGAG 2460
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Db 2461 CACTACTTGCCTTGAATGCTATGCTGACAGGCCCGCAAGAGGTATGCTATGCGAGACC 2520
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Db 2521 CCAATGCAATGCGGATCTTCAACATGATGCAACTAAGGATCACTTCAATCAACCTGAAA 2580
Qy 3473 AAGACATATGCAACCAAGACATTTCAAGATATCTCCCGGCTTGCACACAGCCAGTTA 3532
Db 2581 AAGACATATGCAACCAAGACATTTCAAGATATCTCCCGGCTTGCACACAGCCAGTTA 2640
Qy 3533 CAGCTATTTGATGACACTGACATTACGATGAAAGATGAAACCAAGAACCCGTCAGAA 3592
Db 2641 CAGCTATTTGATGACACTGACATTACGATGAAAGATGAAACCAAGAACCCGTCAGAA 2700
Qy 3593 AGAACATTTGAATCGATATTTACAGGGGCCAAGAAAGCCAGAGCCAGGGATATATCTGTA 3652
Db 2701 AGAACATTTGAATCGATATTTACAGGGGCCAAGAAAGCCAGAGCCAGGGATATATCTGTA 2760
Qy 3653 CATGTTTCGCGGGTGGTTAAGCAATTTGCAATTCAGTATCCCGGACATGAAGTATGA 3712
Db 2761 CATGTTTCGCGGGTGGTTAAGCAATTTGCAATTCAGTATCCCGGACATGAAGTATGA 2820
Qy 3713 CAGCGCGGCTTCAAGAGGCTTAAACAGAAAGAGATGATGCGTCCGCAAAAAGTCA 3772
Db 2821 CAGCGCGGCTTCAAGAGGCTTAAACAGAAAGAGATGATGCGTCCGCAAAAAGTCA 2880
Qy 3773 ATGAAAAACCACTGATCGGATATCATCAGAGATGGAACGTTGTTCAACCCGACATG 3832
Db 2881 ATGAAAAACCACTGATCGGATATCATCAGAGATGGAACGTTGTTCAACCCGACATG 2940
Qy 3833 AGGACAGGCTAGTGTGAAACCTTCAAGGGCGACCATATGATTAAGACAGCCCATATCA 3892
Db 2941 AGGACAGGCTAGTGTGAAACCTTCAAGGGCGACCATATGATTAAGACAGCCCATATCA 3000
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Qy 3953 TTGCTGCATTAACAGCCCACTCCCGTGCCTAATCCGTTCACTGACAGACCAAGCTTT 4012
Db 3061 TTGCTGCATTAACAGCCCACTCCCGTGCCTAATCCGTTCACTGACAGACCAAGCTTT 3120

QY 4013 GCTGGCGAAGACATTGGAAACCGATACAGCAGCGCGGTATGTAATTACCGGTTGCC 4072
Db 3121 GCTGGCGAAGACATTGGAAACCGATACAGCAGCGCGGTATGTAATTACCGGTTGCC 3180
QY 4073 AGTGGAGCGAACTGTTTCCACAGTTTGGGATGACAAACCACTTGGCCATTACGCTT 4132
Db 3181 AGTGGAGCGAACTGTTTCCACAGTTTGGGATGACAAACCACTTGGCCATTACGCTT 3240
QY 4133 TAGACGTAATTGATTAAGTTTTCGGCATGSACTTGACAGGCGA CTGTTTCTAAC 4192
Db 3241 TAGACGTAATTGATTAAGTTTTCGGCATGSACTTGACAGGCGA CTGTTTCTAAC 3300
QY 4193 AGAGCATCCCACTAACGTACCATCCCGCATTCAGCGAGCGCGGTAGCTATTGGACA 4252
Db 3301 AGAGCATCCCACTAACGTACCATCCCGCATTCAGCGAGCGCGGTAGCTATTGGACA 3360
QY 4253 ACAGCCCAAGAACCCGCAAGTATGGTACGATCAAGCCATTGCGCGGAATCTTCCGTA 4312
Db 3361 ACAGCCCAAGAACCCGCAAGTATGGTACGATCAAGCCATTGCGCGGAATCTTCCGTA 3420
QY 4313 GATTTCCGGTGTTCACGTAGCTGGGAAGGGCACAACAATTGATTGAGCGGGGAAA 4372
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QY 4373 CCAGAGTTATCTGCAACAGATTAACCTGTCCTGGTGAACCGGAATCTTCTCAGCGCT 4432
Db 3481 CCAGAGTTATCTGCAACAGATTAACCTGTCCTGGTGAACCGGAATCTTCTCAGCGCT 3540
QY 4433 TAGTCCCGAGTACAAAGAGAAAGCAACCCGCGCGGTCAAAAAATCTTGAACAAGTTCA 4492
Db 3541 TAGTCCCGAGTACAAAGAGAAAGCAACCCGCGCGGTCAAAAAATCTTGAACAAGTTCA 3600
QY 4493 AACCACTCAGTACTTGTGTATCAGAGAAATAATTTGAAGCTCCCGTAAAGAAATCG 4552
Db 3601 AACCACTCAGTACTTGTGTATCAGAGAAATAATTTGAAGCTCCCGTAAAGAAATCG 3660
QY 4553 AATGATTCGCGCCGATGGATGCGGTCGAGTAAGAACTAACACCTGCTTCCGGT 4612
Db 3661 AATGATTCGCGCCGATGGATGCGGTCGAGTAAGAACTAACACCTGCTTCCGGT 3720
QY 4613 TTCCGCGCAGGCAACGATGCACTGTGTTCATCAACTTGAACAATAATACAGAAAC 4672
Db 3721 TTCCGCGCAGGCAACGATGCACTGTGTTCATCAACTTGAACAATAATACAGAAAC 3780
QY 4673 ACCACTTTACGATGCGAAGACATGCGGCGAATTAACCTTTCCGCTTCCGGC 4732
Db 3781 ACCACTTTACGATGCGAAGACATGCGGCGAATTAACCTTTCCGCTTCCGGC 3840
QY 4733 TGAATTGTTAACTCAGGAGGACCCCTGTTGTAAGTCTTATGGCTAACGCGGCA 4792
Db 3841 TGAATTGCTTAACCCAGAGGACCCCTGTTGTAAGTCTTATGGCTAACGCGGCA 3900
QY 4793 ACAATGAGACGTAGTACACCGCTTTGCGCAGAAATTTGTCAGGGTGTCTGACGAGAC 4852
Db 3901 ACAATGAGACGTAGTACACCGCTTTGCGCAGAAATTTGTCAGGGTGTCTGACGAGAC 3960
QY 4853 CAGATTGTCTCAAGCAATACAGAAATGTAATCTGATTTTCCGACAACTAAGCAACAGCC 4912
Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTAATCTGATTTTCCGACAACTAAGCAACAGCC 4020
QY 4913 GTACACGGCAATTAACCCCGGACCATCTGAATTTGGGATTTTCGTCGCTGATAGGGTA 4972
Db 4021 GTACACGGCAATTAACCCCGGACCATCTGAATTTGGGATTTTCGTCGCTGATAGGGTA 4080
QY 4973 CAAGAGATGAGATTGAGCCCGCGCTGATACCGCACCAAAAGGAGAAATTTGCTGACT 5032
Db 4081 CAAGAGATGAGATTGAGCCCGCGCTGATACCGCACCAAAAGGAGAAATTTGCTGACT 4140
QY 5033 GTCAAGAGAAAGCATTTGTCAACGACCAATCCGCTGGTGAACCAAGGAGAGATCT 5092
Db 4141 GTCAAGAGAAAGCATTTGTCAACGACCAATCCGCTGGTGAACCAAGGAGAGATCT 4200

QY 5093 GCGGTGCATCTATTAACGTTTGGCCGACCAAGTTTACCGAATTCACCAACGAGACAGGCA 5152
Db 4201 GCGGTGCATCTATTAACGTTTGGCCGACCAAGTTTACCGAATTCACCAACGAGACAGGCA 4260
QY 5153 CCGCAAGAAATGACGTGTGCTAGGAAAGAAAGATTCACCGCGGTGGCCCTGATTTCC 5212
Db 4261 CCGCAAGAAATGACGTGTGCTAGGAAAGAAAGATTCACCGCGGTGGCCCTGATTTCC 4320
QY 5213 GGAAGCACCAAGAGCAAGACCTTGAATTTGCTACAAAACGCTCAATCAGTGGCAG 5272
Db 4321 GGAAGCACCAAGAGCAAGACCTTGAATTTGCTACAAAACGCTCAATCAGTGGCAG 4380
QY 5273 ACTTATTAATGAACATTAACATCAAGTCTGTGCGCATTCACCTGATCTTACAGCAATTT 5332
Db 4381 ACTTATTAATGAACATTAACATCAAGTCTGTGCGCATTCACCTGATCTTACAGCAATTT 4440
QY 5333 ACGACGCCGAAAAAGACCGCTTGAAGTATCACTTAATCTGTTACAAACCGCGCTAAGCA 5392
Db 4441 ACGACGCCGAAAAAGACCGCTTGAAGTATCACTTAATCTGTTACAAACCGCGCTAAGCA 4500
QY 5393 GAACTGACGGGAGCTAACCATCTATTGCGCTGATTAAGAGTGAAGAAAGAAATCGACG 5452
Db 4501 GAACTGACGGGAGCTAACCATCTATTGCGCTGATTAAGAGTGAAGAAAGAAATCGACG 4560
QY 5453 CGGCACTCCAACTTAAGAGTCTGTAAACAGACTGAAGATGAAGATATGAGATCGACG 5512
Db 4561 CGGCACTCCAACTTAAGAGTCTGTAAACAGACTGAAGATGAAGATATGAGATCGACG 4620
QY 5513 ATGAGTTAGTATGGAATTCATTCAGACAGTGTCTTGAAGGAAAGAAAGGATTCAGTACTA 5572
Db 4621 ATGAGTTAGTATGGAATTCATTCAGACAGTGTCTTGAAGGAAAGAAAGGATTCAGTACTA 4680
QY 5573 CAAAAGGAAATTTATTCGACTTCGAAGGCAACAAATTCATCAAGCAGCAAAAGCA 5632
Db 4681 CAAAAGGAAATTTATTCGACTTCGAAGGCAACAAATTCATCAAGCAGCAAAAGCA 4740
QY 5633 TGGCGAGATTAAGGTCTGTTCCTTAATGACAGAGAAAGTAATGAACAATGTGTGCT 5692
Db 4741 TGGCGAGATTAAGGTCTGTTCCTTAATGACAGAGAAAGTAATGAACAATGTGTGCT 4800
QY 5693 ACATATTTGGGTGAGACATGAGAACAAATCCGGAAGAGTCCCGGTGACCATTAACCGT 5752
Db 4801 ACATATTTGGGTGAGACATGAGAACAAATCCGGAAGAGTCCCGGTGACCATTAACCGT 4860
QY 5753 CGTCAAGCCGCGCAAAACGTTGCGGTGCTTCATGATGATGACATGACGCGCAGAAAGG 5812
Db 4861 CGTCAAGCCGCGCGCAAAACGTTGCGGTGCTTCATGATGATGACATGACGCGCAGAAAGG 4920
QY 5813 TCACAGACTTAAGAGCAATTAACGTCAAGAAAGTTAAGTATGCTCTCCACCCCTTC 5872
Db 4921 TCACAGACTTAAGAGCAATTAACGTCAAGAAAGTTAAGTATGCTCTCTCCACCCCTTC 4980
QY 5873 CTAAGCAAAAATTAAGATGTTCAAGAGTTCAAGTGTGCTCTCCACCCCTTC 5932
Db 4981 CTAAGCAAAAATTAAGATGTTCAAGAGTTCAAGTGTGCTCTCTCCACCCCTTC 5040
QY 5933 CGCACATCCCGGCAATTTGTTCCCGCGGTAAAGTACATTAAGAGTCCAGAAAGCTTACCG 5992
Db 5041 CGCACATCCCGGCAATTTGTTCCCGCGGTAAAGTACATTAAGAGTCCAGAAAGCTTACCG 5100
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Db 5101 CTCCTCTGCAACGAGCGAGAGGCGCCGGAAGTTGTAAGCAGACCGCTACCATCTACAG 5160
QY 6053 CTGATTAACACTGCTTGATGATCAACAGATCTCACTGATATGATGACAGTACGAG 6112
Db 5161 CTGATTAACACTGCTTGATGATCAACAGATCTCACTGATATGATGACAGTACGAG 5220
QY 6113 GCTCACTTTTTCAGACTTTTACCGGATCGGACAACTGATTAATCAATGATGACAGTGGT 6172
Db 5221 GCTCACTTTTTCAGACTTTTACCGGATCGGACAACTGATTAATCAATGATGACAGTGGT 5280
QY 6173 CGTCAGGACCTAGTTCACTAGATAGTATGACCAAGGCAAGGTGTGCTGACGTTCC 6232

Db 5281 CGTCAGACCTGATTCACGTAGATAGTAGACCGAAGGCAAGTGTGGCTGACGTTTC 5340
Qy 6233 ATGCCGCTCCAGAGCCCTGCCCCCTATTCACCGCCAGGCTTAAGAAAGATGGCCGCTGG 6292
Db 5341 ATCCCGCTCCAGAGCCCTGCCCCCTATTCACCGCCAGGCTTAAGAAAGATGGCCGCTGG 5400
Qy 6293 CACGCGCAAAAAAGAGCCCACTCCACCGGCAAGCAATAGCTGATCCCTCCACTCT 6352
Db 5401 CACGCGCAAAAAAGAGCCCACTCCACCGGCAAGCAATAGCTGATCCCTCCACTCT 5460
Qy 6353 CTTTGGTGGGGTATCCATGTCCCTCGGATGCAATTTTCAGACGAGACCGCCGCTGAG 6412
Db 5461 CTTTGGTGGGGTATCCATGTCCCTCGGATGCAATTTTCAGACGAGACCGCCGCTGAG 5520
Qy 6413 CACGCGTACAAACCCCTGGCAACAGGCCCCAGATGTGCTATGTCTTTGGATGCTTTT 6472
Db 5521 CACGCGTACAAACCCCTGGCAACAGGCCCCAGATGTGCTATGTCTTTGGATGCTTTT 5580
Qy 6473 CCGACGAGAGATTGATGAGCTGAGCCGACAGATGATGATCGAACCCTGCTTTT 6532
Db 5581 CCGACGAGAGATTGATGAGCTGAGCCGACAGATGATGATCGAACCCTGCTTTT 5640
Qy 6533 GATCATTTGAAACCGGCGAAAGTGAATCTCAATTATATGTCCTCCATCAGCCGATCTTTT 6592
Db 5641 GATCATTTGAAACCGGCGAAAGTGAATCTCAATTATATGTCCTCCATCAGCCGATCTTTT 5700
Qy 6593 CACTACGCAAGACAGAGCTGAGACGAGAGACGAGAGACTGAATCTGACTAACCGGG 6652
Db 5701 CACTACGCAAGACAGAGCTGAGAGACGAGAGACTGAATCTGACTAACCGGG 5760
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Db 5761 TAGTGGGTATCATATTTTCACGACACAGACCTTGCGCACTTGCAAAAAGAGTCCGTTT 5820
Qy 6713 TGCAGAACCAAGCTTACAGAACCGACCTTGAGCGCAATGTCTTGAAAGAAATTCATGCC 6772
Db 5821 TGCAGAACCAAGCTTACAGAACCGACCTTGAGCGCAATGTCTTGAAAGAAATTCATGCC 5880
Qy 6773 CGGTGCTGACACGTCGAAAGAGAACAACTCAAGTACAGATGATGCGCACG 6832
Db 5881 CGGTGCTGACACGTCGAAAGAGAACAACTCAAGTACAGATGATGATGCGCACG 5940
Qy 6833 AAGCCAAACAAAAGTAGTACAGTCTCGTAAAGTAGAATAACAGAAAGCATTAACA 6892
Db 5941 AAGCCAAACAAAAGTAGTACAGTCTCGTAAAGTAGAATAACAGAAAGCATTAACA 6000
Qy 6893 AGCGACTACTGTGAGACTACAGACTGATTAATCTTGCCACAGATCAGCCAGATGCTATA 6952
Db 6001 AGCGACTACTGTGAGACTACAGACTGATTAATCTTGCCACAGATCAGCCAGATGCTATA 6060
Qy 6953 AGATCACTTATCGAAACCAATTTACTGACGATAGCGTACCGGCAACTACCTCCGATCAC 7012
Db 6061 AGATCACTTATCGAAACCAATTTACTGACGATAGCGTACCGGCAACTACCTCCGATCAC 6120
Qy 7013 AGTTGCGTGTAGTGTCTGTAAACAATATCTGATGAGAACTATCCGACAGTACATCTT 7072
Db 6121 AGTTGCGTGTAGTGTCTGTAAACAATATCTGATGAGAACTATCCGACAGTACATCTT 6180
Qy 7073 ATCAGATTACTGACGAGTACGATGCTTAATTGATATGATGACGAGACAGTGGCATGCC 7132
Db 6181 ATCAGATTACTGACGAGTACGATGCTTAATTGATATGATGAGAGGAGCAAGTCCCTGCC 6240
Qy 7133 TGGATTAATGCAACCTTTCGCGCGCTAAGCTTAAGTTACCGAAAAAATAGATATA 7192
Db 6241 TGGATTAATGCAACCTTTCGCGCGCTAAGCTTAAGTTACCGAAAAAATAGATATA 6300
Qy 7193 GAGCCCGGAATATCCGACAGTGGTTCATCAGAGATGACAGAACGCTCAAAAATGTGC 7252
Db 6301 GAGCCCGGAATATCCGACAGTGGTTCATCAGAGATGACAGAACGCTCAAAAATGTGC 6360
Qy 7253 TCATTGCGGCACTTAAGAAATTGCAAGTCAAGCAGATGCTGAACTGCCACA 7312
Db 6361 TCATTGCGGCACTTAAGAAATTGCAAGTCAAGCAGATGCTGAACTGCCACA 6420
Qy 7313 ACTACGCAATTCATCATGTGATGCTTTCGAAAATATCATGTATGACGATATTGG 7372
Db 6421 ACTACGCAATTCATCATGTGATGCTTTCGAAAATATCATGTATGACGATATTGG 6480
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Db 6481 AGGAGTTCCCTGGAAAGCCCAATTAGATTACATGATGTTTGTACCCGATATGTAAGCTA 6540
Qy 7433 GACTGAAGGCCCTAAGCGCGCGCATTAATTTGCAAAAAGCTAATATTTGGTCCCATTCG 7492
Db 6541 GACTGAAGGCCCTAAGCGCGCGCATTAATTTGCAAAAAGCTAATATTTGGTCCCATTCG 6600
Qy 7493 AAGAAATGCTTATGATATGATTCATGATGATGATGATGATGATGATGATGATGATGATG 7552
Db 6601 AAGAAATGCTTATGATATGATTCATGATGATGATGATGATGATGATGATGATGATGATG 6660
Qy 7553 GCACGAAACACACAGAAAGAACCGAAGTACAGATGATACAGCCCGCAAAACCCCTGG 7612
Db 6661 GCACGAAACACACAGAAAGAACCGAAGTACAGATGATACAGCCCGCAAAACCCCTGG 6720
Qy 7613 CGACTGCTTACTTATGCGGGATTTACCGGGAAATTAGTGGTGGCTTACCGCCGCTTGG 7672
Db 6721 CGACTGCTTACTTATGCGGGATTTACCGGGAAATTAGTGGTGGCTTACCGCCGCTTGG 6780
Qy 7673 TTCCAAACATTCACACGCTTTTTCACATGTCCGCGAGAGATTTGATGCAATATGACAG 7732
Db 6781 TTCCAAACATTCACACGCTTTTTCACATGTCCGCGAGAGATTTGATGCAATATGACAG 6840
Qy 7733 AACACTTCAAGCAAGCGCACCCGCTTCTGAGACGGAATTCGATATTCGACAAAAGCC 7792
Db 6841 AACACTTCAAGCAAGCGCACCCGCTTCTGAGACGGAATTCGATATTCGACAAAAGCC 6900
Qy 7793 AAGACGACGCTAAGGAGTTAACCGGTCTGATGATCTTGAGAGACTGGGTGTGATCAAC 7852
Db 6901 AAGACGACGCTAAGGAGTTAACCGGTCTGATGATCTTGAGAGACTGGGTGTGATCAAC 6960
Qy 7853 CACTACTGACCTTATGAGTGGCGCTTTTGAGAAATATCATCACCATCTACCTACCG 7912
Db 6961 CACTACTGACCTTATGAGTGGCGCTTTTGAGAAATATCATCACCATCTACCTACCG 7020
Qy 7913 GTACTGTTTAAATTCGGGGCGATGATGAATTCGGAATGTTCCTACACTTTTGTCA 7972
Db 7021 GTACTGTTTAAATTCGGGGCGATGATGAATTCGGAATGTTCCTACACTTTTGTCA 7080
Qy 7973 ACAAGTTTGAATGCTTATGCGCAGCAGATACAGAAAGAGCGGCTTAACGCTCA 8032
Db 7081 ACAAGTTTGAATGCTTATGCGCAGCAGATACAGAAAGAGCGGCTTAACGCTCA 7140
Qy 8033 GATGTGAGCGTTCATTTGGCGACGACAACTATCATGAGATGATATCTGACAAAAGAA 8092
Db 7141 GATGTGAGCGTTCATTTGGCGACGACAACTATCATGAGATGATATCTGACAAAAGAA 7200
Qy 8093 TGGCTGAGAGTGGCGCATCTGCTCAACATGAGGTTAAGATCATGACGAGTATCG 8152
Db 7201 TGGCTGAGAGTGGCGCATCTGCTCAACATGAGGTTAAGATCATGACGAGTATCG 7260
Qy 8153 GTGAGAGACCACTTACTTGTGCGGCGAATTAATCTTGCAAGATTCGGTACTTCCAG 8212
Db 7261 GTGAGAGACCACTTACTTGTGCGGCGAATTAATCTTGCAAGATTCGGTACTTCCAG 7320
Qy 8213 CGTGGCGGTGGCGGATCCCTGTAAGAAAGCTGTTTAAGTTGGGTAAACCGCTCCAGCCG 8272
Db 7321 CGTGGCGGTGGCGGATCCCTGTAAGAAAGCTGTTTAAGTTGGGTAAACCGCTCCAGCCG 7380
Qy 8273 ACAGACGACAAACGAAAGACAGAAAGAGCGCTCTGCTAATGAAACAAAGCGGTGTTA 8332
Db 7381 ACAGACGACAAACGAAAGACAGAAAGAGCGCTCTGCTAATGAAACAAAGCGGTGTTA 7440
Qy 8333 GAGTAGGTATTAACAGGCACTTTCAGTGGCGGTGACGACCCGGTATGAGGTAGACATA 8392
Db 7441 GAGTAGGTATTAACAGGCACTTTCAGTGGCGGTGACGACCCGGTATGAGGTAGACATA 7500

QY 8393 TTACACCTGTCCTACTGCGATTGAGAACTTTGGCCAGAGCAAAAGACATTCCAGCCA 8452
DB 7501 TTACACCTGTCCTACTGCGATTGAGAACTTTGGCCAGAGCAAAAGACATTCCAGCCA 7560
QY 8453 TCAGAGGGGAAATTAAGCATCTTACGGTGGTCTCTAATATAGTCAGCATAGTACATTTTCAT 8512
DB 7561 TCAGAGGGGAAATTAAGCATCTTACGGTGGTCTCTAATATAGTCAGCATAGTACATTTTCAT 7620
QY 8513 CTGACTATATACTACACACGACCACT 8539
DB 7621 CTGACTATATACTACACACGACCACT 7647

RESULT 11

ID ABRN86686 standard; DNA; 9951 BP.
AC ABRN86686;

DT 05-NOV-2002 (first entry)
XX

DE Nucleotide sequence of a SINreps self replicating replicon.

KM Major histocompatibility complex; MHC; antigen presenting cell; APC;
KM antigen; cytotoxic; virulence; gene therapy; CD8; vaccine; therapeutic;
KM cancer; viral infection; ds.

OS Synthetic.

PN WO200261113-A2.

PD 08-AUG-2002.

PF 01-FEB-2002; 2002WO-US002598.

PR 01-FEB-2001; 2001US-0265334P.

PA (UYUO) UNIV JOHNS HOPKINS.

PI Wu T, Hung C;

DR WPI; 2002-619261/66.

PT Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as vaccine
PT for cancer and viral infections.

PS Claim 27; Page 23-25; 127pp; English.

XX The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-P) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of a SINreps self replicating replicon

XX Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 893 ATTGACGGCGTAGTACACACTATTGAAATCAAAACGCCGACCAATGTGACATCAACA 952
DB 1 ATTGACGGCGTAGTACACACTATTGAAATCAAAACGCCGACCAATGTGACATCAACA 60
QY 953 TGGAGAAAGCCAGTAGTAAAGCTAGACGTAGACCCCCAGAGTCGGTTGTCTGCAACTGC 1012
DB 61 TGGAGAAAGCCAGTAGTAAAGCTAGACGTAGACCCCCAGAGTCGGTTGTCTGCAACTGC 120
QY 1013 AAAAAGCTTCCCGCAATTTAGGTAGTACAGACAGAGGTCACTCCAAATGACCATGTGTA 1072
DB 121 AAAAAGCTTCCCGCAATTTAGGTAGTACAGACAGAGGTCACTCCAAATGACCATGTGTA 180
QY 1073 ATGCGAAGACATTTTGCATCTGCGCAGTAACTAATGAGCTGAGAGTTCTTACACAG 1132
DB 181 ATGCGAAGACATTTTGCATCTGCGCAGTAACTAATGAGCTGAGAGTTCTTACACAG 240
QY 1133 CGACGATCTTGGACATAGGACAGCGCACCGGCTCGTAGAATTTTCCGAGACCAATATC 1192
DB 241 CGACGATCTTGGACATAGGACAGCGCACCGGCTCGTAGAATTTTCCGAGACCAATATC 300
QY 1193 ATTGATCTGCCCCGATGCGTAGTCCAGAAAGCCCGGACCGGATGTAATGACGACAGTA 1252
DB 301 ATTGATCTGCCCCGATGCGTAGTCCAGAAAGCCCGGACCGGATGTAATGACGACAGTA 360
QY 1253 AACTGCGGAAAAAGCGTGCAGATTAACAACAAGAACTTGCATGAGAAAGATTAGATC 1312
DB 361 AACTGCGGAAAAAGCGTGCAGATTAACAACAAGAACTTGCATGAGAAAGATTAGATC 420
QY 1313 TCCGGAACCGTACTTGATACGCGGATGCTGAACAACCATCGCTCTGCTTTCACAACGATG 1372
DB 421 TCCGGAACCGTACTTGATACGCGGATGCTGAACAACCATCGCTCTGCTTTCACAACGATG 480
QY 1373 TTACCTGCAACATGCGGCGGAAATATTCGGTATGCGAGGAGATGATATCAACGCTCCG 1432
DB 481 TTACCTGCAACATGCGGCGGAAATATTCGGTATGCGAGGAGATGATATCAACGCTCCG 540
QY 1433 GAACATCTATCATCAGGCTATGAAAGCGTGCAGACCTGTGATGATGAGCTTTCGACA 1492
DB 541 GAACATCTATCATCAGGCTATGAAAGCGTGCAGACCTGTGATGATGAGCTTTCGACA 600
QY 1493 CCACCCAGTTGATGTTCTCGGCTATGCGAGTTGTAACCTGCGTACACAACCACTGGG 1552
DB 601 CCACCCAGTTGATGTTCTCGGCTATGCGAGTTGTAACCTGCGTACACAACCACTGGG 660
QY 1553 CCGACGGAAGATGCTTGAAGCGGCTAACATCGGACTTTGAGACAAAGCTGAGTAG 1612
DB 661 CCGACGGAAGATGCTTGAAGCGGCTAACATCGGACTTTGAGACAAAGCTGAGTAG 720
QY 1613 GTAGACAGAAATTTGTCATATGAGAAAGAGATTGAACCCGCGGTCCGCGGTTT 1672
DB 721 GTAGACAGAAATTTGTCATATGAGAAAGAGATTGAACCCGCGGTCCGCGGTTT 780
QY 1673 ATTTCTCGTAGATGCACTTTATCCAGAACAGAGCCAGCTTGACAGCTGGCATC 1732
DB 781 ATTTCTCGTAGATGCACTTTATCCAGAACAGAGCCAGCTTGACAGCTGGCATC 840
QY 1733 TTCCATGCGTCTTCCACTGTAATGGAAGCAAGTGTACCTTGGCGCTGTGATACAGTGG 1792
DB 841 TTCCATGCGTCTTCCACTGTAATGGAAGCAAGTGTACCTTGGCGCTGTGATACAGTGG 900
QY 1793 TGAATTCGAAAGGCTAGTAGTGAAGAAATCACCATCAGTCCGCGGATCAAGGAGAA 1852
DB 901 TGAATTCGAAAGGCTAGTAGTGAAGAAATCACCATCAGTCCGCGGATCAAGGAGAA 960
QY 1853 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTTGCTATGCAAAAGTTACTGACA 1912
DB 961 CCGTGGATACGCGGTTACACACAATAGCGAGGCTTCTTGCTATGCAAAAGTTACTGACA 1020
QY 1913 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTCAAGTACATCCGCGCACCAATATGCG 1972
DB 1021 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTCAAGTATCCGCGCACCAATATGCG 1080
QY 1973 ATCAGATGACTGTGTATATGCGCACGAGATATATCATCCTGACGATGACAAAAACTTGG 2032

1081 ATCGATGACTGATATATGCGACGATATATACCTGACGATGCAAAAACTTTG 1140
QY TTGGGCTCAACCAAGCAATTTGCTATTAACGGTAGACTTAAACAGAACCAACCACTATG 2092
Db TTGGGCTCAACCAAGCAATTTGCTATTAACGGTAGACTTAAACAGAACCAACCACTATG 1200
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Db ATGATCTTGATTAACGAGAAAACTGGGTACTAGAGAACGCAAGCTTAACGATGGCTGCT 1320
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Db GCGTAAAGTCCCGACTTTTATGCGCTTTTCCCATGTGCTCGTATGACGACTCTT 1440
QY TGCCCATGTGCTGAGGAGCAAAATTTGAACTGGATGCAACCAAGAGAGAGAGAAAC 2392
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QY TGCTGACGATCTCGAGGAAATTAGTCAATGAGGCAAGGCTGCTTTGAGAGATGCTCAG 2452
Db TGCTGACGATCTCGAGGAAATTAGTCAATGAGGCAAGGCTGCTTTGAGAGATGCTCAG 1560
QY AGGAAAGCAAGCGGAGAAAGCTCCGAGAGCACTTCCACCTTATGTCGACCAAGGCA 2512
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Db TCGAGGAGCGCGAGAGTTGTCTGCGAGTGAAGGGGCTCCAGGGGAGCATCGAGACAG 1621
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QY TCGGACAGTATATGCTGTCTCGCCAACTCTGTGCTGAAGAAATGCGCAACCTGCAACAG 2692
Db TCGGACAGTATATGCTGTCTCGCCAACTCTGTGCTGAAGAAATGCGCAACCTGCAACAG 1741
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Db AATTCCTAGACCTGAGAGAGCGCCCTTAAGTATCAACGAAAGAGATTTGTGAAC 2041
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2161 ATCATGAGTACGCTCGAGAGGAGCTGAAGACCCGACCTGCGGTCCGTTACAAGGTGAAA 2220
QY CAATAGAGTATAGGACACACCGGGGTCCGGCAAGTCAAGCTATTAATCAAGTCACTGTC 3113
Db CAATAGAGTATAGGACACACCGGGGTCCGGCAAGTCAAGCTATTAATCAAGTCACTGTC 2221
QY CGGACAGAGATCTTGTTCACAGCGGAAAGAAATTTGTCCCGAAATTTAGGCGGACG 3232
Db CGGACAGAGATCTTGTTCACAGCGGAAAGAAATTTGTCCCGAAATTTAGGCGGACG 2281
QY TGCTAAGACTGAGGGGATGACAGATTAACGTGCAAGACAGTATGCTATGCTCAAG 3292
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Db CACTACTTGTGCTGATTTGCTATGTCAGGCCCCGCAAGAGGTAATCTATGCGAGACC 2461
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QY AAGACATATGACCAAGACATTTCTACAGTATATCTCCGCGCTTGCACACAGCCAGTTA 3532
Db AAGACATATGACCAAGACATTTCTACAGTATATCTCCGCGCTTGCACACAGCCAGTTA 2581
QY AAGACATATGACCAAGACATTTCTACAGTATATCTCCGCGCTTGCACACAGCCAGTTA 3592
Db AAGACATATGACCAAGACATTTCTACAGTATATCTCCGCGCTTGCACACAGCCAGTTA 2641
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QY GCTGGGCGAAAGCATTTGAAACCGATTAAGCAACGAGCGGATTCGTTTACCGGTTGCC 4072
Db GCTGGGCGAAAGCATTTGAAACCGATTAAGCAACGAGCGGATTCGTTTACCGGTTGCC 3121
QY AGTGAAGCAACTGTTCCCAAGTTTGGGATGACAAACCAATTTGGCATTTAGCCTT 4132
Db AGTGAAGCAACTGTTCCCAAGTTTGGGATGACAAACCAATTTGGCATTTAGCCTT 4073
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Db AGTGAAGCAACTGTTCCCAAGTTTGGGATGACAAACCAATTTGGCATTTAGCCTT 4133
QY TAGACGTAATTTGATTAAGTTTTCGAGCATGAGACTTGAACAGCGGACTGTTTCAAAC 4192
Db TAGACGTAATTTGATTAAGTTTTCGAGCATGAGACTTGAACAGCGGACTGTTTCAAAC 3241

QY 4193 AGAGCATCCCACTAAGTACATCCGCCGATTACGGAGGCGGTAGCTGATTGGACA 4252
DB 3301 AGAGCATCCCACTAAGTACATCCGCCGATTACGGAGGCGGTAGCTGATTGGACA 3360
QY 4253 ACAGCCAGGAAACCGGAGATGGGTACGATCAAGCATTTGGCGGCAATCTCCGTA 4312
DB 3361 ACAGCCAGGAAACCGGAGATGGGTACGATCAAGCATTTGGCGGCAATCTCCGTA 3420
QY 4313 GATTTCCGATGTTCCAGCTAGCTGGGAAAGGACACAATTTGATTTGAGACGGGAGAA 4372
DB 3421 GATTTCCGATGTTCCAGCTAGCTGGGAAAGGACACAATTTGATTTGAGACGGGAGAA 3480
QY 4373 CCAGATTATCTGCAACAGATTAAGCTGTCGGGTGAACCGCAATCTTCTCAAGCT 4432
DB 3481 CCAGATTATCTGCAACAGATTAAGCTGTCGGGTGAACCGCAATCTTCTCAAGCT 3540
QY 4433 TAGTCCCGAGTACAAAGGAAAGCAACCGGCCGCTCAAAAATTTCTGAACCAAGTTCA 4492
DB 3541 TAGTCCCGAGTACAAAGGAAAGCAACCGGCCGCTCAAAAATTTCTGAACCAAGTTCA 3600
QY 4493 AACCACTAGTACTGTTGATCAGAGGAAATAATGAAGTCCCGTAAAGAAATG 4552
DB 3601 AACCACTAGTACTGTTGATCAGAGGAAATAATGAAGTCCCGTAAAGAAATG 3660
QY 4553 AATGATCGCCCGATTGGCATAGCCGCTGAGATTAAGAACTAAGCTGCTTCCGCT 4612
DB 3661 AATGATCGCCCGATTGGCATAGCCGCTGAGATTAAGAACTAAGCTGCTTCCGCT 3720
QY 4613 TTCCGCGGAGGACCGGTGACCTGTTGATCAACATTTGAACTAAATACGAAACC 4672
DB 3721 TTCCGCGGAGGACCGGTGACCTGTTGATCAACATTTGAACTAAATACGAAACC 3780
QY 4673 ACCACTTACGAGTGGAGAACCATGGGACCTTAAAAACCTTCCGCTCCGCGCC 4732
DB 3781 ACCACTTACGAGTGGAGAACCATGGGACCTTAAAAACCTTCCGCTCCGCGCC 3840
QY 4733 TGAATGTTAACTCAGAGGACCCCTGTTGAAAGTCTTATGAGCTACGCGACGCA 4792
DB 3841 TGAATGTTAACTCAGAGGACCCCTGTTGAAAGTCTTATGAGCTACGCGACGCA 3960
QY 4793 ACAGTGAAGACGTAGTACCGCTTTGGCAGAAAGTTGTGACGGGTGTCTGACGAGAC 4852
DB 3901 ACAGTGAAGACGTAGTACCGCTTTGGCAGAAAGTTGTGACGGGTGTCTGACGAGAC 3960
QY 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGCAACTAGACAAAGCC 4912
DB 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGCAACTAGACAAAGCC 4020
QY 4913 GTACACGGCAATTCACCCGACCATCTGAATTCGATGATTTGCTCGGTGTATAGGGTA 4972
DB 4021 GTACACGGCAATTCACCCGACCATCTGAATTCGATGATTTGCTCGGTGTATAGGGTA 4080
QY 4973 CAAGAGATGAGTGGAGCGCGCGCTATACGACCAAAAAGGAGAAATTTCTGACT 5032
DB 4081 CAAGAGATGAGTGGAGCGCGCGCTATACGACCAAAAAGGAGAAATTTCTGACT 4140
QY 5033 GTCAAGAGAGAGCTGTCTCAAGCAGCAATCCGCTGGGTAGACCAAGGCAAGAGTCT 5092
DB 4141 GTCAAGAGAGAGCTGTCTCAAGCAGCAATCCGCTGGGTAGACCAAGGCAAGAGTCT 4200
QY 5093 GCGGTGCATCTATAAAGTTGGCGGACAGTTTATCCGATTCAGCCACGGAGCAGGCA 5152
DB 4201 GCGGTGCATCTATAAAGTTGGCGGACAGTTTATCCGATTCAGCCACGGAGCAGGCA 4260
QY 5153 CCGGAGAAATGACTGTGCTTGAAGAAAGAAAGTATCCAGCGCTGCGCTGATTTCC 5212
DB 4261 CCGGAGAAATGACTGTGCTTGAAGAAAGAAAGTATCCAGCGCTGCGCTGATTTCC 4320
QY 5213 GGAAGCAACCGAAGAGAGCTTTGAATTTGCTACAAACGCTTACATGAGTGAG 5272
DB 4321 GGAAGCAACCGAAGAGAGCTTTGAATTTGCTACAAACGCTTACATGAGTGAG 4380

QY 5273 ACTTAGTAATGAAATTAACATCAAGTCTGCGGCAATTCAGCTGCTATCTACAGCAATT 5332
DB 4381 ACTTAGTAATGAAATTAACATCAAGTCTGCGGCAATTCAGCTGCTATCTACAGCAATT 4440
QY 5333 ACAGAGCCGGAAGAACCGCTTGAAGTATCATCTTAAGCTTGAACAACCGCTAGACA 5392
DB 4441 ACAGAGCCGGAAGAACCGCTTGAAGTATCATCTTAAGCTTGAACAACCGCTAGACA 4500
QY 5393 GAACTGACGGGAGCTAACCATCTATTGCTGATTAAGAGTGAAGGAAAGAAATGACG 5452
DB 4501 GAACTGACGGGAGCTAACCATCTATTGCTGATTAAGAGTGAAGGAAAGAAATGACG 4560
QY 5453 CGGACCTCCAACTTAAGAGCTCTTAACAGAGCTGAAGAGTGAAGTATGAGATCCAGC 5512
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QY 5573 CAAAGGAAATTTGATTTCTGACTTGAAGGACCAAAATTCATCAAGCAGCAAAAAGCA 5632
DB 4681 CAAAGGAAATTTGATTTCTGACTTGAAGGACCAAAATTCATCAAGCAGCAAAAAGCA 4740
QY 5633 TGGCGAGATTAAGGCTCTGTTCCCTAATGACAGAGAAAGTATGAACAATCTGTGCT 5692
DB 4741 TGGCGAGATTAAGGCTCTGTTCCCTAATGACAGAGAAAGTATGAACAATCTGTGCT 4800
QY 5693 ACATATTGGGTGAACCATGGAACCAATCCGCGAAAGTGGCCGCTGACATACATACCGT 5752
DB 4801 ACATATTGGGTGAACCATGGAACCAATCCGCGAAAGTGGCCGCTGACATACATACCGT 4860
QY 5753 CGTCTAGCCGCGCAAAAAGTTGCGGCTGTCATGATGATGATGATGATGATGATGATG 5812
DB 4861 CGTCTAGCCGCGCAAAAAGTTGCGGCTGTCATGATGATGATGATGATGATGATGATG 4920
QY 5813 TCACAGACTTGAAGAAATTAAGCAATCAAGAAAGTTAAGTGTCTCCACCCCTTC 5872
DB 4921 TCACAGACTTGAAGAAATTAAGCAATCAAGAAAGTTAAGTGTCTCCACCCCTTC 4980
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DB 4981 CTAAAGCAAAATTTAAGATTTTGAAGAGTTGATGATGATGATGATGATGATGATGATG 5040
QY 5933 CGCACATCCCGCAATTTGCTCCGCGCTAAGTATCAATGAAGTGCAGAACGCTACCG 5992
DB 5041 CGCACATCCCGCAATTTGCTCCGCGCTAAGTATCAATGAAGTGCAGAACGCTACCG 5100
QY 5993 CTCCTCTGACAGGCGAGAGGCGCCGCAAGTTGTAGCGACACCGTCAACATCTACAG 6052
DB 5101 CTCCTCTGACAGGCGAGAGGCGCCGCAAGTTGTAGCGACACCGTCAACATCTACAG 5160
QY 6053 CTGATTAACCTCGCTGATGTCAAGACATCTCACTGATATGATGATGATGATGATGATG 6112
DB 5161 CTGATTAACCTCGCTGATGTCAAGACATCTCACTGATATGATGATGATGATGATGATG 5220
QY 6113 GCTACCTTTTGAAGCTTGAAGCGGATCGACATCTATTAAGTATGATGATGATGATG 6172
DB 5221 GCTACCTTTTGAAGCTTGAAGCGGATCGACATCTATTAAGTATGATGATGATGATG 5280
QY 6173 CGTCAAGACCTAAGTTCACTAGATAGTATGACCAAGGAGAGTGTGTGCTGACGTTCC 6232
DB 5281 CGTCAAGACCTAAGTTCACTAGATAGTATGACCAAGGAGAGTGTGTGCTGACGTTCC 5340
QY 6233 ATGCGTCCAAAGACTGCGCTTATTCACCGGCAAGCTTAAGAAAGTGGCCGCTGG 6292
DB 5341 ATGCGTCCAAAGACTGCGCTTATTCACCGGCAAGCTTAAGAAAGTGGCCGCTGG 5400
QY 6293 CAGCGGCAAGAAAGACCCATCCACCGGGAAGCAATAGCTGAGTCCCTCCACCTCT 6352
DB 5401 CAGCGGCAAGAAAGACCCATCCACCGGGAAGCAATAGCTGAGTCCCTCCACCTCT 5460
QY 6353 CTTTGTGGGGTATCATATGCTCGGATCAATTTTGCAGGAGAGACGGCCGCGCAG 6412

Db 5461 CTTTGGTGGGATATCATATGCTCCCTCGATCAATTTTCAGCGAGACGCGCCGCGCAGG 5520
Qy 6413 CACGGGTACAAACCCCTGGCAACAGGCCCAACGGATGTCCTATGTCCTTTGGATCGTTTT 6472
Db 5521 CACGGGTACAAACCCCTGGCAACAGGCCCAACGGATGTCCTATGTCCTTTGGATCGTTTT 5580
Qy 6473 CCGACGAGAGATTTGATGAGCTGAGCGCGAGATTAATGATCCGAACCCGTCCTGTTTG 6532
Db 5581 CCGACGAGAGATTTGATGAGCTGAGCGCGAGATTAATGATCCGAACCCGTCCTGTTTG 5640
Qy 6533 GATCATTTGAAACCGGCGGAAGTGAATCATTTATATGTCCTCGATCAGCCGTAATCTTTTC 6592
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Qy 6593 CACTACGCAAGACAGAGCTGAGACGAGAGACGAGAGACTGAATCTGACTAACCGGG 6652
Db 5701 CACTACGCAAGACAGAGCTGAGACGAGAGACGAGAGACTGAATCTGACTAACCGGG 5760
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Db 5761 TAGGTGGGTACATATTTTCAGCGGACACAGGCCCTGGGCACTTGCAGAAAGAGTCGTTTC 5820
Qy 6713 TGGAGAACCGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAAATTCATGCCC 6772
Db 5821 TGGAGAACCGCTTACAGAACCGACCTTGGAGCGCAATGTCCTGGAAAGAAATTCATGCCC 5880
Qy 6773 CGGTGCTCGACAGTGCAGAAAGAGAACCACTCAAACTCAGGTACAGATGATGATGCCACG 6832
Db 5881 CGGTGCTCGACAGTGCAGAAAGAGAACCACTCAAACTCAGGTACAGATGATGATGCCACG 5940
Qy 6833 AAGCCAAAGAAAGTACAGTACAGTCTGTAAGTAGAAATCAGAAAGCCATTAACAATG 6892
Db 5941 AAGCCAAAGAAAGTACAGTACAGTCTGTAAGTAGAAATCAGAAAGCCATTAACAATG 6000
Qy 6893 AAGGACTACTGTCAGAGCTACAGTGTATACTCTGCCACAGATCAGCCGGAATGCTATA 6952
Db 6001 AAGGACTACTGTCAGAGCTACAGTGTATACTCTGCCACAGATCAGCCGGAATGCTATA 6060
Qy 6953 AGATCAACCTTCCGAAACCAATTTGATCTCCAGTAGCGTACCGGCAATCTCCGATCCAG 7012
Db 6061 AGATCAACCTTCCGAAACCAATTTGATCTCCAGTAGCGTACCGGCAATCTCCGATCCAG 6120
Qy 7013 AGTTGCTGAGTGTCTGTATACAACTATCTGATGAGAACTATCCGACAGTAGCATCTT 7072
Db 6121 AGTTGCTGAGTGTCTGTATACAACTATCTGATGAGAACTATCCGACAGTAGCATCTT 6180
Qy 7073 ATCAGATTACTGACGAGTACGATGCTTACCTTGATATGATGACGAGACGTCGCTGCC 7132
Db 6181 ATCAGATTACTGACGAGTACGATGCTTACCTTGATATGATGACGAGACGTCGCTGCC 6240
Qy 7133 TGGATACGCAACTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAATCATGAGATA 7192
Db 6241 TGGATACGCAACTTCTGCCCCGCTAAGCTTAGAAGTTACCCGAAAAAATCATGAGATA 6300
Qy 7193 GAGCCCCGAAATATCCGAGTGCAGTTCATCAGCGATGCAAGAACGCTTCAAAAATGTCG 7252
Db 6301 GAGCCCCGAAATATCCGAGTGCAGTTCATCAGCGATGCAAGAACGCTTCAAAAATGTCG 6360
Qy 7253 TCAATTCGCGCACTTAAAGAAATTTGCAACGTCACGCAAGTGCCTGCAACACTGG 7312
Db 6361 TCAATTCGCGCACTTAAAGAAATTTGCAACGTCACGCAAGTGCCTGCAACACTGG 6420
Qy 7313 ACTCAGGACATTCATGTCGAATGCTTGCAGAAATATGATGATGACGAGATTTGG 7372
Db 6421 ACTCAGGACATTCATGTCGAATGCTTGCAGAAATATGATGATGACGAGATTTGG 6480
Qy 7373 AGGAGTTCCGTCGGAAGCAATTAGATTAACAATGATTTGTACCGCATATGATGATA 7432
Db 6481 AGGAGTTCCGTCGGAAGCAATTAGATTAACAATGATTTGTACCGCATATGATGATA 6540
Qy 7433 GACTGAAGGCCCTTAAGCCGCGCATATTTGCAAGAGATTAATTTGGTCCCATGTC 7492

Db 6541 GACTGAAGGCCCTTAAGCCGCGCATATTTGCAAGAGATTAATTTGGTCCCATGTC 6600
Qy 7493 AAGAAATGCTCTATGATAGATTCGATGAGACATGAAAAAGAGAGCTGAAGTATACACAG 7552
Db 6601 AAGAAATGCTCTATGATAGATTCGATGAGACATGAAAAAGAGAGCTGAAGTATACACAG 6660
Qy 7553 GCACGAAACACACAGAAAGAAAGCCGAAAGTACAGATGATCAAGCCGCAAGAACCCCTGG 7612
Db 6661 GCACGAAACACACAGAAAGAAAGCCGAAAGTACAGATGATCAAGCCGCAAGAACCCCTGG 6720
Qy 7613 CGATGCTCTTATATGCGGGATTCACCGGGAATTAAGGTAGGCTTACCGCGCTGTCG 7672
Db 6721 CGATGCTCTTATATGCGGGATTCACCGGGAATTAAGGTAGGCTTACCGCGCTGTCG 6780
Qy 7673 TTCCAAACATTCACACGCTTTTGTGACATGTCGCGAGAGATTTTGTATGCAATCATGACAG 7732
Db 6781 TTCCAAACATTCACACGCTTTTGTGACATGTCGCGAGAGATTTTGTATGCAATCATGACAG 6840
Qy 7733 AACACTTCAAGCAAGCGCACCCGCTGATGAGACGAGATATCCGATCATTCGACAAAGCC 7792
Db 6841 AACACTTCAAGCAAGCGCACCCGCTGATGAGACGAGATATCCGATCATTCGACAAAGCC 6900
Qy 7793 AAGACGAGCTATGCGGTTTAAACCGGTCTGATGATCTTGGAGAGCTGGGTGGATCAAC 7852
Db 6901 AAGACGAGCTATGCGGTTTAAACCGGTCTGATGATCTTGGAGAGCTGGGTGGATCAAC 6960
Qy 7853 CACTACTCGACTTGATGAGTGCAGTGCCTTTGAGAAATATCATCACCACATCTACTACG 7912
Db 6961 CACTACTCGACTTGATGAGTGCAGTGCCTTTGAGAAATATCATCACCACATCTACTACG 7020
Qy 7913 GTACTGCTTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTTCAACTTTTGTCA 7972
Db 7021 GTACTGCTTTTAAATTCGGGGCGATGATGAATCCGGAATGTTCTTCAACTTTTGTCA 7080
Qy 7973 ACACAGTTTGAATGTCGTTATGCGGACAGAGTACTGAAGAGCGGCTTAAAGCCCA 8032
Db 7081 ACACAGTTTGAATGTCGTTATGCGGACAGAGTACTGAAGAGCGGCTTAAAGCCCA 7140
Qy 8033 GATGTCAGCGTTCATTTGCGAGACGACAAATCATCATGAGAGTATCTGACAAAGAA 8092
Db 7141 GATGTCAGCGTTCATTTGCGAGACGACAAATCATCATGAGAGTATCTGACAAAGAA 7200
Qy 8093 TGGCTGAGAGTGCAGCCTGCTCAACATGAGGTTAAGATCATGACGACGATCG 8152
Db 7201 TGGCTGAGAGTGCAGCCTGCTCAACATGAGGTTAAGATCATGACGACGATCG 7260
Qy 8153 GTGAGAGCAACCTTACTCTGCGGCGATTTATCTTGAAGATGCGGTACTTCCACAG 8212
Db 7261 GTGAGAGCAACCTTACTCTGCGGCGATTTATCTTGAAGATGCGGTACTTCCACAG 7320
Qy 8213 CGTGCGCGTGCAGATCCCTGAAAAAGCTGTTTAAAGTTGGTAAACCGCTCCAGCCG 8272
Db 7321 CGTGCGCGTGCAGATCCCTGAAAAAGCTGTTTAAAGTTGGTAAACCGCTCCAGCCG 7380
Qy 8273 ACAGAGAGCAAGACGAAAGACGAAAGCGCTTGTCTAGATGAACAAAGGCTGGTTTA 8332
Db 7381 ACAGAGAGCAAGACGAAAGACGAAAGCGCTTGTCTAGATGAACAAAGGCTGGTTTA 7440
Qy 8333 GAGTAGTATTAACAGGCACTTTAGCAGTGGCGGTGAAGACCCGCTTATGAGGTAGACATA 8392
Db 7441 GAGTAGTATTAACAGGCACTTTAGCAGTGGCGGTGAAGACCCGCTTATGAGGTAGACATA 7500
Qy 8393 TTACACTGTCCTACTAGGATGAGAACTTTTGGCCAGAGCAAAAGACATTCAGAGCCA 8452
Db 7501 TTACACTGTCCTACTAGGATGAGAACTTTTGGCCAGAGCAAAAGACATTCAGAGCCA 7560
Qy 8453 TCAGAGGGGAATTAAGCATCTTACGCGTGTCTTAAATGTCAGCATAGTACATTTTCAT 8512
Db 7561 TCAGAGGGGAATTAAGCATCTTACGCGTGTCTTAAATGTCAGCATAGTACATTTTCAT 7620
Qy 8513 CTGACTTAATTAACAACACACACACCT 8539
Db 7621 CTGACTTAATTAACAACACACACACCT 7647

RESULT 12
ABV73174
ID ABV73174 standard; DNA; 9951 BP.
XX
AC ABV73174;
XX
DT 08-JAN-2003 (first entry)
XX
DE Nucleotide sequence of Sindbis self replicating replicon.
XX
KM Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
XX hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; ds.
XX
OS Sindbis virus.
XX
PN W0200274920-A2.
XX
PD 26-SEP-2002.
XX
PF 18-MAR-2002; 2002MO-US008033.
XX
PR 16-MAR-2001; 2001US-0276854P.
XX
PA (UYJO) UNIV JOHNS HOPKINS.
XX
PI Wu T, Hung C;
XX
DR WPI; 2002-740856/80.
XX
PT New nucleic acid molecule encoding an antigenic fusion polypeptide useful
PT as vaccines for enhancing or inducing immune responses, primarily
PT cytotoxic T lymphocytes (CTL) responses to specific antigens such as
PT tumor or viral antigens.
XX
PS Disclosure; Page 56-58; 93bp; English.
XX
XX The invention relates to a nucleic acid molecule that encodes a fusion
CC polypeptide, comprising a first nucleic acid sequence encoding a
CC polypeptide that comprises at least one immunogenicity-potentiating
CC polypeptide, optionally, fused in frame with the nucleic acid, a linker
CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked
CC in frame to them, and that encodes an antigenic peptide or polypeptide.
CC The nucleic acid molecule, polypeptides and vectors are useful as
CC vaccines for enhancing immune responses, primarily cytotoxic T
CC lymphocytes (CTL) responses to specific antigens such as tumour or viral
CC antigens, and for inhibiting growth or preventing re-growth of a tumour.
CC The packaging cell line is useful for generating alphavirus replicon
CC particles without contamination from replicon-competent virus. The
CC pathogenic organisms include viruses such as human papilloma virus (HPV),
CC hepatitis B virus, hepatitis C virus, human immunodeficiency virus,
CC Epstein Barr virus and herpes simplex virus, intracellular parasites such
CC as malaria, and bacteria that grow intracellularly such as mycobacteria
CC and listeria. The present sequence represents the nucleotide sequence of
CC the sindbis virus RNA replicon vector Sindrep5, a self replicating
CC replicon
XX
SQ Sequence 9951 BP; 2852 A; 2460 C; 2465 G; 2174 T; 0 U; 0 Other;
Query Match 89.4%; Score 7637.4; DB 6; Length 9951;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 893 ATTGACGGCGTATGATACACATTTGATCAAAACAGCCGACCAATTGCACTACATCAAA 952
DB 1 ATTACCGCGGTATGACACATTTGATCAAAACAGCCGACCAATTGCACTACATCAAA 60
QY 953 TGGAGAGCCGATGTAAACGTAGACGAGACCCCGACAGTCCGTTTCCGTGCAACTGC 1012
DB 61 TGGAGAGCCGATGTAAACGTAGACGAGACCCCGACAGTCCGTTTCCGTGCAACTGC 120
QY 1013 AAAAAGCTTCCCGCAATTGAGTAGAGACAGACAGTCACTCAATGACCATGCTA 1072

DB 121 AAAAAGCTTCCCGCAATTGAGTAGAGACAGACAGTCACTCAATGACCATGCTA 180
QY 1073 ATGCGAGAGCATTTTGCATCTGGCCAGTAACTAATGAGCTGAGAGTCTCTACACAG 1132
DB 181 ATGCGAGAGCATTTTGCATCTGGCCAGTAACTAATGAGCTGAGAGTCTCTACACAG 240
QY 1133 CGACGATCTTGGACATAGGACCGCACCGGCTCGTAGAATTTTCCGAGCACAAGATC 1192
DB 241 CGACGATCTTGGACATAGGACCGCACCGGCTCGTAGAATTTTCCGAGCACAAGATC 300
QY 1193 ATTGTCTGCCCCATGCGTATGTCGAGAGACCCGAGCCGATGTAATATCCGCACTA 1252
DB 301 ATTGTCTGCCCCATGCGTATGTCGAGAGACCCGAGCCGATGTAATATCCGCACTA 360
QY 1253 AACTGGGGGAAAAAGCGTGAAGATTTCAAACAGAACTTSCATGAGAAAGTTAAGATC 1312
DB 361 AACTGGGGGAAAAAGCGTGAAGATTTCAAACAGAACTTSCATGAGAAAGTTAAGATC 420
QY 1313 TCCGAGACCGTACTTGAATACGCGGATGCTGAACACCATCGCTGCTTTCACAACGATG 1372
DB 421 TCCGAGACCGTACTTGAATACGCGGATGCTGAACACCATCGCTGCTTTCACAACGATG 480
QY 1373 TTACCTGCAACATGCGTGCAGATATTTCCGTATGACAGACGCTGTATCAACGCTCCG 1432
DB 481 TTACCTGCAACATGCGTGCAGATATTTCCGTATGACAGACGCTGTATCAACGCTCCG 540
QY 1433 GAACATCTATCATCAGGCTATGAAAGCGCGGACCCCTGACTGATGGCTTCGACA 1492
DB 541 GAACATCTATCATCAGGCTATGAAAGCGCGGACCCCTGACTGATGGCTTCGACA 600
QY 1493 CCACCCAGTTGATGTTCTCGGCTATGAGCAAGTTCGTACCTGCGTACCAACCAACTGG 1552
DB 601 CCACCCAGTTGATGTTCTCGGCTATGAGCAAGTTCGTACCTGCGTACCAACCAACTGG 660
QY 1553 CCGACGAGAAAGTCTTGAAGCGCGTAAACATCGAATTGTCAGACAACAAAGCTGAGTAA 1612
DB 661 CCGACGAGAAAGTCTTGAAGCGCGTAAACATCGAATTGTCAGACAACAAAGCTGAGTAA 720
QY 1613 GTAGACAGAGAAATTTGTCGTAATGAGAAAGAGTTAAAGCCCGGTCGCGGTTT 1672
DB 721 GTAGACAGAGAAATTTGTCGTAATGAGAAAGAGTTAAAGCCCGGTCGCGGTTT 780
QY 1673 ATTCTCCGTGAGATTCGACATTTATCCAGAACACAGGCCAGCTTGAGACCTGCAATC 1732
DB 781 ATTCTCCGTGAGATTCGACATTTATCCAGAACACAGGCCAGCTTGAGACCTGCAATC 840
QY 1733 TTCCATCGGTGTTCACTTGAATGAAAGCAGTGTACCTTGCCTGTGATACAGTGG 1792
DB 841 TTCCATCGGTGTTCACTTGAATGAAAGCAGTGTACCTTGCCTGTGATACAGTGG 900
QY 1793 TGAAGTGGAGAGGCTAGCTAGTAAAGAAATCACATTAAGTCCCGGATTCACGGAGAA 1852
DB 901 TGAAGTGGAGAGGCTAGCTAGTAAAGAAATCACATTAAGTCCCGGATTCACGGAGAA 960
QY 1853 CCGTGGGATTAAGCGGTTTACACAAATAGCGAGGCTTTCTGCTATGCAAAAGTTACTGACA 1912
DB 961 CCGTGGGATTAAGCGGTTTACACAAATAGCGAGGCTTTCTGCTATGCAAAAGTTACTGACA 1020
QY 1913 CAGTAAAGAGAAACGGGTATGTTCCCTGTGTGACGATACATCCCGGACCAATATGCG 1972
DB 1021 CAGTAAAGAGAAACGGGTATGTTCCCTGTGTGACGATACATCCCGGACCAATATGCG 1080
QY 1973 ATCAGATGATCGGTATATAGGCGACAGATATATCACTGACGAGATGCAAAAACTTCTGG 2032
DB 1081 ATCAGATGATCGGTATATAGGCGACAGATATATCACTGACGAGATGCAAAAACTTCTGG 1140
QY 2033 TTGGGCTCAACACAGCAATTTGTCAATTAACGCTAGACGTAACAGAAACCAACACATGCG 2092
DB 1141 TTGGGCTCAACACAGCAATTTGTCAATTAACGCTAGACGTAACAGAAACCAACACATGCG 1200
QY 2093 AAAATTACCTTCTGCGCATATAGACCAAGGTTTCAAGAAATGGCTTAAGAGCGCAAG 2152

Dh 1201 AAAATTAACCTTCTGCGCATATACACAGGGTTCAAGCAAAATGGGCTAAGAGCGCAAG 1260
Qy 2153 ATGATCTTGAATTAACGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGATGCTGCT 2212
Dh 1261 ATGATCTTGAATTAACGAGAAAAATGCTGGGTACTAGAGAACGCAAGCTTACGATGCTGCT 1320
Qy 2213 TGTGGGCGTTTCGCACTAAGAAATGACATTTGTTTATCGCCCACTGGAAACGCAAGCT 2272
Dh 1321 TGTGGGCGTTTCGCACTAAGAAATGACATTTGTTTATCGCCCACTGGAAACGCAAGCT 1380
Qy 2273 GCGTAAAGTCCCGAGCTCTTTTACGCTTTTCCCATGCTGCTCGTATGACGACCTCTT 2332
Dh 1381 GCGTAAAGTCCCGAGCTCTTTTACGCTTTTCCCATGCTGCTCGTATGACGACCTCTT 1440
Qy 2333 TGCCCATGCTGCTGAGGCGAGAAATTTGAAACTGCGATTGCAACCAAGAGAGAGAAAAAC 2392
Dh 1441 TGCCCATGCTGCTGAGGCGAGAAATTTGAAACTGCGATTGCAACCAAGAGAGAGAAAAAC 1500
Qy 2393 TGCTGCAAGTCTCGAGAGAAATTAATGCAATGAGGCCAAGGCTGCTTTTGAAGATGCTCAGG 2452
Dh 1501 TGCTGCAAGTCTCGAGAGAAATTAATGCAATGAGGCCAAGGCTGCTTTTGAAGATGCTCAGG 1560
Qy 2453 AGGAAAGCAGAGGCGAGAGAGTCCGAGAGACCTTCCACATTAATGAGCGAGACAAAGGCA 2512
Dh 1561 AGGAAAGCAGAGGCGAGAGAGTCCGAGAGACCTTCCACATTAATGAGCGAGACAAAGGCA 1620
Qy 2513 TCGAGGCGAGCGCGAGAGTTGTCTGCGAAGTGAAGGGGCTTCAAGCGGAGCATCGAGCAG 2572
Dh 1621 TCGAGGCGAGCGCGAGAGTTGTCTGCGAAGTGAAGGGGCTTCAAGCGGAGCATCGAGCAG 1680
Qy 2573 CATTAATTGAAACCCCGCGGCTCAAGTAAGATTAATCTCAAGCAATGACCGTATGA 2632
Dh 1681 CATTAATTGAAACCCCGCGGCTCAAGTAAGATTAATCTCAAGCAATGACCGTATGA 1740
Qy 2633 TCGGACAGTATATGTTGTCTCGCCCAACTCTGCTGAGAGAAATGGCAAACTCGACACAG 2692
Dh 1741 TCGGACAGTATATGTTGTCTCGCCCAACTCTGCTGAGAGAAATGGCAAACTCGACACAG 1800
Qy 2693 CGGACCCGCTAGCAGATCAGGTTAAGATCAATACACACTCCGGAAGATCAGAAAGTACG 2752
Dh 1801 CGGACCCGCTAGCAGATCAGGTTAAGATCAATACACACTCCGGAAGATCAGAAAGTACG 1860
Qy 2753 CGGTCGACCATACGAGCGCTTAAATGATCTGATGCCAGAGAGGGTCCGTCATGCGCAG 2812
Dh 1861 CGGTCGACCATACGAGCGCTTAAATGATCTGATGCCAGAGAGGGTCCGTCATGCGCAG 1920
Qy 2813 AATTCTAGCAGCTGAGTGAAGCGCCAGTTAGTGAAGCAAGAGAGGTTTGTGAAC 2872
Dh 1921 AATTCTAGCAGCTGAGTGAAGCGCCAGTTAGTGAAGCAAGAGAGGTTTGTGAAC 1980
Qy 2873 GCAAACTATACACATTTGCCATGATGAGCCCGCCCAAGAAATACAGAGAGAGCATAC 2932
Dh 1981 GCAAACTATACACATTTGCCATGATGAGCCCGCCCAAGAAATACAGAGAGAGCATAC 2040
Qy 2933 AGGTTACAAAGGCGAGCTTGCAGAAACAGAGTACGTTTGAAGCTGAGCAAGAGGTT 2992
Dh 2041 AGGTTACAAAGGCGAGCTTGCAGAAACAGAGTACGTTTGAAGCTGAGCAAGAGGTT 2100
Qy 2993 GCGTTAAGAGAGAGAGCTCAGGCTGCTGCTCTCGGAGAACTGACCAACCTCCCT 3052
Dh 2101 GCGTTAAGAGAGAGAGCTCAGGCTGCTGCTCTCGGAGAACTGACCAACCTCCCT 2160
Qy 3053 ATCATAGAGTACTGCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTTACAAAGTGCAAA 3112
Dh 2161 ATCATAGAGTACTGCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTTACAAAGTGCAAA 2220
Qy 3113 CAATAGAGAGTATAGGACACACCGGGGTCGGGCAAGTACGTTATTAAGTCAACTGTCA 3172
Dh 2221 CAATAGAGAGTATAGGACACACCGGGGTCGGGCAAGTACGTTATTAAGTCAACTGTCA 2280
Qy 3173 CGGACGAGATCTTGTATACGAGCGGAAAGAAATTTGTCGGAATTTGAGGCGGAG 3232
Dh 2281 CGGACGAGATCTTGTATACGAGCGGAAAGAAATTTGTCGGAATTTGAGGCGGAG 2340

Qy 3233 TGCTAAGACTGAGGGGTATATGCAATTAACGTCGAAGACAGTATGCTATGCTCAACG 3292
Dh 2341 TGCTAAGACTGAGGGGTATATGCAATTAACGTCGAAGACAGTATGCTATGCTCAACG 2400
Qy 3293 GATGCCAACAAGCCGTAGAAATGCTGTACGTTGACGAAGCGTTCCGCTGCGACGAGAG 3352
Dh 2401 GATGCCAACAAGCCGTAGAAATGCTGTACGTTGACGAAGCGTTCCGCTGCGACGAGAG 2460
Qy 3353 CACTACTGCTGATGCTATGCTATGCTAGAGCGCCCGCAAGAGATGATCTATGCGAGAC 3412
Dh 2461 CACTACTGCTGATGCTATGCTATGCTAGAGCGCCCGCAAGAGATGATCTATGCGAGAC 2520
Qy 3413 CCATGCAATGCGGATTTCTTCAACATGATGCACTAAAGGATCAATTCACCTGAAA 3472
Dh 2521 CCATGCAATGCGGATTTCTTCAACATGATGCACTAAAGGATCAATTCACCTGAAA 2580
Qy 3473 AAGACATATGACCAAGACATTTCTACAGTATATCTCCCGGCTTGACACAGCCAGTTA 3532
Dh 2581 AAGACATATGACCAAGACATTTCTACAGTATATCTCCCGGCTTGACACAGCCAGTTA 2640
Qy 3533 CAGCTATTGATGACACTGCACTTACGATGGAAGATGAACCAAGAACCCGTTGCAAGA 3592
Dh 2641 CAGCTATTGATGACACTGCACTTACGATGGAAGATGAACCAAGAACCCGTTGCAAGA 2700
Qy 3593 AGAACATTTGAATCGATATTTACAGGGGCCCAAAAGCCGAAGCCAGGAGATATCATCTGA 3652
Dh 2701 AGAACATTTGAATCGATATTTACAGGGGCCCAAAAGCCGAAGCCAGGAGATATCATCTGA 2760
Qy 3653 CATGTTCCGCGGGTGGTTAAGCAATTTGCAATTCGATATCCCGGACATGAAGTATGA 3712
Dh 2761 CATGTTCCGCGGGTGGTTAAGCAATTTGCAATTCGATATCCCGGACATGAAGTATGA 2820
Qy 3713 CAGCGGCGCTCACAAAGGGCTTAACGAGAAAGAGATGATGCGTCCGCGCAAAAAGTCA 3772
Dh 2821 CAGCGGCGCTCACAAAGGGCTTAACGAGAAAGAGATGATGCGTCCGCGCAAAAAGTCA 2880
Qy 3773 ATGAAACCCCACTGTACGCGATCATCATAGAGATGAAACGTTGCTTCAACCCGACTG 3832
Dh 2881 ATGAAACCCCACTGTACGCGATCATCATAGAGATGAAACGTTGCTTCAACCCGACTG 2940
Qy 3833 AGGACAGCTATGATGGAACAACTTGCAGAGGCGACCCATGAGATTAAGACGCCCATAC 3892
Dh 2941 AGGACAGCTATGATGGAACAACTTGCAGAGGCGACCCATGAGATTAAGACGCCCATAC 3000
Qy 3893 TACCTAAAGAACTTCAAGGCTACTATAGAGACTGAGGAGCTGGAACCAAGGAATA 3952
Dh 3001 TACCTAAAGAACTTCAAGGCTACTATAGAGACTGAGGAGCTGGAACCAAGGAATA 3060
Qy 3953 TTGCTGCAATTAACAGCCCACTCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT 4012
Dh 3061 TTGCTGCAATTAACAGCCCACTCCCGTGCCAATCCGTTCACTGCAAGACCAACGTTT 3120
Qy 4013 GCTGGGCGAAAGATTTGGAACCGATCTAGCCACGCGCGGTATCTGATCTTAACGGTTGCC 4072
Dh 3121 GCTGGGCGAAAGATTTGGAACCGATCTAGCCACGCGCGGTATCTGATCTTAACGGTTGCC 3180
Qy 4073 AGTGAAGCAACTGTTCCCAAGTTTGCAGATGACAAACCACTATGCGGCAATTAAGCCT 4132
Dh 3181 AGTGAAGCAACTGTTCCCAAGTTTGCAGATGACAAACCACTATGCGGCAATTAAGCCT 3240
Qy 4133 TAGACGTAATTTGATTAAGTTTTCGAGATGACTTGAACAAGCGGACTGTTTCTTAAC 4192
Dh 3241 TAGACGTAATTTGATTAAGTTTTCGAGATGACTTGAACAAGCGGACTGTTTCTTAAC 3300
Qy 4193 AAGGCAATCCCACTAAGTACATCCCGCGGATTTACGCGAGCGCGGTATGAGTCAATGGAGCA 4252
Dh 3301 AAGGCAATCCCACTAAGTACATCCCGCGGATTTACGCGAGCGCGGTATGAGTCAATGGAGCA 3360
Qy 4253 ACAGCCGAGAAACCCGCAAGTATGAGTACATCAAGCAATTTGCGCGGCAACTCTCCGTA 4312
Dh 3361 ACAGCCGAGAAACCCGCAAGTATGAGTACATCAAGCAATTTGCGCGGCAACTCTCCGTA 3420

QY 4313 GATTCCGGTGTTCAGCTAGCTGGGAAGGCAACAACCTTGATTTGGACGCGGAGAA 4372
DB 3421 GATTCCGGTGTTCAGCTAGCTGGGAAGGCAACAACCTTGATTTGGACGCGGAGAA 3480
QY 4373 CCAAGTATATCTGCACAGCATTAACCGGTCCGGGGAACCGGAATTTCTCTACAGCCT 4432
DB 3481 CCAAGTATATCTGCACAGCATTAACCGGTCCGGGGAACCGGAATTTCTCTACAGCCT 3540
QY 4433 TAGTCCCGGAGTACAGAGAGAGCAACCCGGCCGGTCAAAAAATTTCTTGAACCAAGTTCA 4492
DB 3541 TAGTCCCGGAGTACAGAGAGAGCAACCCGGCCGGTCAAAAAATTTCTTGAACCAAGTTCA 3600
QY 4493 AACCACTCAGTACTTGTTGTATCAGAGAAAAAATTTGAAGTCTCCCGTAAAGAAATCG 4552
DB 3601 AACCACTCAGTACTTGTTGTATCAGAGAAAAAATTTGAAGTCTCCCGTAAAGAAATCG 3660
QY 4553 AATGATCGCCCGATGGGATAGCCGGTGAATTAAGAACTAACACCTGGCTTTCCGGGT 4612
DB 3661 AATGATCGCCCGATGGGATAGCCGGTGAATTAAGAACTAACACCTGGCTTTCCGGGT 3720
QY 4613 TTCCGCGGAGGCAAGGATCAGCTGTGTTCAATCAATTTGAATTAATACAGAAACC 4672
DB 3721 TTCCGCGGAGGCAAGGATCAGCTGTGTTCAATCAATTTGAATTAATACAGAAACC 3780
QY 4673 ACCACTTTCAGCAGTGCAGAGACCATGCGGACCTTAAAAACCTTTTCGGGTTCCGGCC 4732
DB 3781 ACCACTTTCAGCAGTGCAGAGACCATGCGGACCTTAAAAACCTTTTCGGGTTCCGGCC 3840
QY 4733 TGAATTTGTTAACTCAGAGAGGCAACCTGCTGTGTGAAGTCTTAATGGCTAACCCGCA 4792
DB 3841 TGAATTTGTTAACTCAGAGAGGCAACCTGCTGTGTGAAGTCTTAATGGCTAACCCGCA 3900
QY 4793 ACAAGTGAAGAGTATGTCACCGCTCTTGCCAGAAAGTTGTCAAGGTTGTCTCAGCGAGAC 4852
DB 3901 ACAAGTGAAGAGTATGTCACCGCTCTTGCCAGAAAGTTGTCAAGGTTGTCTCAGCGAGAC 3960
QY 4853 CAGATTTGTCTCAAGCAATACAGAAATGTAACCTGATTTTCGCAACAATAGACAACAGCC 4912
DB 3961 CAGATTTGTCTCAAGCAATACAGAAATGTAACCTGATTTTCGCAACAATAGACAACAGCC 4020
QY 4913 GTACACGGCAATTCACCCCGGACCATCTGAATTTGCTGTGATTTGAGGGTA 4972
DB 4021 GTACACGGCAATTCACCCCGGACCATCTGAATTTGCTGTGATTTGAGGGTA 4080
QY 4973 CAAGAGATGAGTGGAGCGCGCGCTCATACCGGACCAAAAAGGAGAAATTTGCTGACT 5032
DB 4081 CAAGAGATGAGTGGAGCGCGCGCTCATACCGGACCAAAAAGGAGAAATTTGCTGACT 4140
QY 5033 GTCAAGAGAGCAAGTGTCAACGACGCAATCCGCTGGTGAACAGGCGAAGAGTCT 5092
DB 4141 GTCAAGAGAGCAAGTGTCAACGACGCAATCCGCTGGTGAACAGGCGAAGAGTCT 4260
QY 5093 GCGCTGCATCTTAATAACGTTGGCCGACAGTTTACCGATTCAAGCCAAGGACAAGGCA 5152
DB 4261 GCGCTGCATCTTAATAACGTTGGCCGACAGTTTACCGATTCAAGCCAAGGACAAGGCA 4260
QY 5153 GCGGCAAGATGACTGTGCTAGAGAAAGAAAGTATCAACGCGGTGGCCCTGATTTCC 5212
DB 4261 GCGGCAAGATGACTGTGCTAGAGAAAGAAAGTATCAACGCGGTGGCCCTGATTTCC 4320
QY 5213 GGAAGCAACCCAGAGAGAGAGCCCTTGAATTTGCTACAAAACGCTACCATCAGTGGAG 5272
DB 4321 GGAAGCAACCCAGAGAGAGAGCCCTTGAATTTGCTACAAAACGCTACCATCAGTGGAG 4380
QY 5273 ACTTAGTAATGAACATTAACATCAAGTGTGTGCGCATTTCACTGCTATCTACAGCAATTT 5332
DB 4381 ACTTAGTAATGAACATTAACATCAAGTGTGTGCGCATTTCACTGCTATCTACAGCAATTT 4440
QY 5333 ACGGAGCGGAGAAAGACCGGCTTGAAGTATCACTTAAGTGAACAACCGCGCTAGACA 5392
DB 4441 ACGGAGCGGAGAAAGACCGGCTTGAAGTATCACTTAAGTGAACAACCGCGCTAGACA 4500
QY 5393 GAACGTACGCGGAGGTAACCATCTATTGCTGTGATTAAGAAAGTGAAGAAAGAAATTCGACG 5452

DB 4501 GAACGTACGCGGAGGTAACCATCTATTGCTGTGATTAAGAAAGTGAAGAAAGAAATTCGACG 4560
QY 5453 CCGCACTTCAACTTAAGAGAGTCTGTACAGAGCTGAAGAGATGAAGATATGAGATTCGACG 5512
DB 4561 CCGCACTTCAACTTAAGAGAGTCTGTACAGAGCTGAAGAGATGAAGATATGAGATTCGACG 4620
QY 5513 ATGAGTTAGTATGAGATTCATCCAGACAGTTGCTTGAAGGAGAAAGGAAATTCAGTACTA 5572
DB 4621 ATGAGTTAGTATGAGATTCATCCAGACAGTTGCTTGAAGGAGAAAGGAAATTCAGTACTA 4680
QY 5573 CAAAAGGAAATTTGATTTCTGATCTTGAAGGACCAAAATTCATCAAGCAGCAAAAGACA 5632
DB 4681 CAAAAGGAAATTTGATTTCTGATCTTGAAGGACCAAAATTCATCAAGCAGCAAAAGACA 4740
QY 5633 TGGCGAGATTAAGGTCCTGTTCCCTAATGACAGAGAAAGTAAAGCAACTGTGTGCT 5692
DB 4741 TGGCGAGATTAAGGTCCTGTTCCCTAATGACAGAGAAAGTAAAGCAACTGTGTGCT 4800
QY 5693 ACATATTTGGGTGAGACCATGGAAGCAATCCGCAAAAAGTCCCGGTGACCATTAACCGGT 5752
DB 4801 ACATATTTGGGTGAGACCATGGAAGCAATCCGCAAAAAGTCCCGGTGACCATTAACCGGT 4860
QY 5753 CGTCTAGCCGCGCCAAAACGTTGCTGCTCTTGCATGATGCCATGACCGCAAGAAAGG 5812
DB 4861 CGTCTAGCCGCGCCAAAACGTTGCTGCTCTTGCATGATGCCATGACCGCAAGAAAGG 4920
QY 5813 TTCCACACTTAAGAGCAATTAAGTCAAGAAAGTAAAGTATGCTCTCCCAACCCCGCTTC 5872
DB 4921 TTCCACACTTAAGAGCAATTAAGTCAAGAAAGTAAAGTATGCTCTCCCAACCCCGCTTC 4980
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QY 5933 CGCACACTCCCGCAATTCGTTCCCGCCGTAAGTACATGAAGTCCAGAAAGAGCCTACCG 5992
DB 5041 CGCACACTCCCGCAATTCGTTCCCGCCGTAAGTACATGAAGTCCAGAAAGAGCCTACCG 5100
QY 5993 CTCCTCGTGAACAGCGGAGAGAGGCCCCGAAAGTTGAAGCAACCGTCAACATCTACAG 6052
DB 5101 CTCCTCGTGAACAGCGGAGAGAGGCCCCGAAAGTTGAAGCAACCGTCAACATCTACAG 5160
QY 6053 CTGATTAACACTCCCTTGATGTCAACAGATCTCACTGATATGATGAACAGTACGAG 6112
DB 5161 CTGATTAACACTCCCTTGATGTCAACAGATCTCACTGATATGATGAACAGTACGAG 5220
QY 6113 GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACTGATTTACTAGATGAGAGTGGT 6172
DB 5221 GCTCACTTTTTCGAGCTTTAGCGGATCGGACAACTGATTTACTAGATGAGAGTGGT 5280
QY 6173 CGTGAAGACTTAAGTCACTAGATATGAGATCGAAGCGAGGTGTGTGCTACAGTTC 6232
DB 5281 CGTGAAGACTTAAGTCACTAGATATGAGATCGAAGCGAGGTGTGTGCTACAGTTC 5340
QY 6233 ATGCGGTCAAGAGCTGCGCCCTATTCACACCGCAAGGCTTAAGAAAGTGGCCGCGCTGG 6292
DB 5341 ATGCGGTCAAGAGCTGCGCCCTATTCACACCGCAAGGCTTAAGAAAGTGGCCGCGCTGG 5400
QY 6293 CAGCGGAGAGAAAGAGCCCACTCAACCGGACCAATAGCTGAGTCCCTCCACCTCT 6352
DB 5401 CAGCGGAGAGAAAGAGCCCACTCAACCGGACCAATAGCTGAGTCCCTCCACCTCT 5460
QY 6353 CTTTGTGGGGGTATCCATGTCCTCGGATCAATTTTTCAGAGAGAGAGCGCCCGCAAG 6412
DB 5461 CTTTGTGGGGGTATCCATGTCCTCGGATCAATTTTTCAGAGAGAGAGCGCCCGCAAG 5520
QY 6413 CAGCGGTACAAACCTCTGAGCAAGGCGCCCAAGATGAGTGGCTATGCTTTCGAGATGTTTT 6472
DB 5521 CAGCGGTACAAACCTCTGAGCAAGGCGCCCAAGATGAGTGGCTATGCTTTCGAGATGTTTT 5580
QY 6473 CCGAGAGAGATTTGATGAGTGAAGCGCAGAGATTAAGTGAAGCCGCTCTGTTTTG 6532

Dp	5581	CCGACGGAGAAATTGATGAGCTGAGCCGACAGATAACTGAGTCCGAACCCGCTGTTTG	5640
Qy	6533	GATCATTTTGAACCGGGGGAAAGTGAATCTCAATTATATGTCCTCCCATGACGGTATCTTTTC	6592
Dp	5641	GATCATTTTGAACCGGGGGAAGTGAATCTCAATTATATGTCCTCCCATGACGGTATCTTTTC	5700
Qy	6593	CACTAACGCAACAGACAGTAGACGACAGGACAGAGAGACTGAATTACTGACTAAACGGAGG	6652
Dp	5701	CACTAACGCAACAGACAGTAGACGACAGGACAGAGAGACTGAATTACTGACTAAACGGAGG	5760
Qy	6653	TAGGTGGGTACATATTTTTCGACGGACACAGGCGCTGGGCACTTTCGAAAGAAGTCCGTTTC	6712
Dp	5761	TAGGTGGGTACATATTTTTCGACGGACACAGGCGCTGGGCACTTTCGAAAGAAGTCCGTTTC	5820
Qy	6713	TGCGAACAACGCTTAAACAGAACCCGACTTTGGAGCCGCAATGTCCTTGGAAGAATTCATGCC	6772
Dp	5821	TGCGAACAACGCTTAAACAGAACCCGACTTTGGAGCCGCAATGTCCTTGGAAGAATTCATGCC	5880
Qy	6773	CGGAGCTCGACAGCTCCGAAAGAGGAACAACCTCAAACTCAGGTACAGATGATGCGCCACCG	6832
Dp	5881	CGGAGCTCGACAGCTCCGAAAGAGGAACAACCTCAAACTCAGGTACAGATGATGCGCCACCG	5940
Qy	6833	AAGCCAAACAAAAGTAGGTAAACGAGTCTGTTAAAGTAGAAATCAGAAAAGCCATAACCACTG	6892
Dp	5941	AAGCCAAACAAAAGTAGGTAAACGAGTCTGTTAAAGTAGAAATCAGAAAAGCCATAACCACTG	6000
Qy	6893	AGCGACTATCTGTCAAGACTACGACTGTATTAATCTGTCCACAGATCAGCCAGATGCTATA	6952
Dp	6001	AGCGACTATCTGTCAAGACTACGACTGTATTAATCTGTCCACAGATCAGCCAGATGCTATA	6060
Qy	6953	AGATCACTTAATCCGAAACCAATTGTAATCTCACTACAGTACCGTACCGGCGAATCACTCCGATCCAC	7012
Dp	6061	AGATCACTTAATCCGAAACCAATTGTAATCTCACTACAGTACCGTACCGGCGAATCACTCCGATCCAC	6120
Qy	7013	AGTTGCGTGTAGCTGTCTGTAAACAATACTGTGATGAGAACTATCCGACAGTACATCTT	7072
Dp	6121	AGTTGCGTGTAGCTGTCTGTAAACAATACTGTGATGAGAACTATCCGACAGTACATCTT	6180
Qy	7073	ATCAGATTACTGACGAGTAGTACGATGCTTAATTGATATGTGTAAGACGAGACAGTGCATGCC	7132
Dp	6181	ATCAGATTACTGACGAGTAGTACGATGCTTAATTGATATGTGTAAGACGAGACAGTGCATGCC	6240
Qy	7133	TGGATTACTGCAACCTTCTGCCCCCGCTAAGCTTAAGAATTAACCGGAAAAACATAGATTA	7192
Dp	6241	TGGATTACTGCAACCTTCTGCCCCCGCTAAGCTTAAGAATTAACCGGAAAAACATAGATTA	6300
Qy	7193	GAGCCCCGAAATATCCGACGAGTCCGGTTCATACAGGATGCAGAAACAGCTAACAAATGTGC	7252
Dp	6301	GAGCCCCGAAATATCCGACGAGTCCGGTTCATACAGGATGCAGAAACAGCTAACAAATGTGC	6360
Qy	7253	TCATTGCGCGAATTAAGAAATTGCAACGTCACGCGAGATCGTGAATCTGCCAACACTGG	7312
Dp	6361	TCATTGCGCGAATTAAGAAATTGCAACGTCACGCGAGATCGTGAATCTGCCAACACTGG	6420
Qy	7313	ACTCAGCGAATTCATATGTGCAATGCTTTCGAAAATATGATGTATATGACAGATATTGGG	7372
Dp	6421	ACTCAGCGAATTCATATGTGCAATGCTTTCGAAAATATGATGTATATGACAGATATTGGG	6480
Qy	7373	AGGAGTTGCGTCGGAAAGCCAAATTAGATTACACTGAGTTTGTCACGCGCATATGTAGCTA	7432
Dp	6481	AGGAGTTGCGTCGGAAAGCCAAATTAGATTACACTGAGTTTGTCACGCGCATATGTAGCTA	6540
Qy	7433	GACTGAAGAGCCCTTAAGGCGCGCACTATTTGCAAGAAGCCGTATATTTGGTCCCATTTGC	7492
Dp	6541	GACTGAAGAGCCCTTAAGGCGCGCACTATTTGCAAGAAGCCGTATATTTGGTCCCATTTGC	6600
Qy	7493	AAGAAATGCTATGTGATATGATTCGTCAATGACATGAAAAGACGTTGAATTAACAACG	7552
Dp	6601	AAGAAATGCTATGTGATATGATTCGTCAATGACATGAAAAGACGTTGAATTAACAACG	6660
Qy	7553	GCACGAAACACACAGAAAGAACCGGAAGTACAAAGTATCAAGCCGACAAACCCCTGG	7612
Dp	6661	GCACGAAACACACAGAAAGAACCGGAAGTACAAAGTATCAAGCCGACAAACCCCTGG	6720

QY	7613	CGACTGCTTACTTAATGGGGGAAATTCAACCGGGAAATTAGATGCTAAGGCTTAACGGCGCTTTGC	7612
Db	6721	CGACTGCTTACTTAATGGGGGAAATTCAACCGGGAAATTAGATGCTAAGGCTTAACGGCGCTTTGC	6780
QY	7673	TTCCAAACATTCAACACGCTTTTGTGACATGTCGGCGGAGATTTTGTATGCAATCATATACAG	7732
Db	6781	TTCCAAACATTCAACACGCTTTTGTGACATGTCGGCGGAGATTTTGTATGCAATCATATACAG	6840
QY	7733	AACACTTCAAGCAAGGCGACCCGGTACTGGAAGACGATATCGCATCATTTGACAAAAGCC	7792
Db	6841	AACACTTCAAGCAAGGCGACCCGGTACTGGAAGACGATATCGCATCATTTGACAAAAGCC	6900
QY	7793	AAGACGACGCTAATGGCGCTTAACCGGCTGATATCTTGGAGAGACCTGGGTGGATGCAC	7852
Db	6901	AAGACGACGCTAATGGCGCTTAACCGGCTGATATCTTGGAGAGACCTGGGTGGATGCAC	6960
QY	7853	CACACTCTCGACTTGATGCGATGCGCCCTTTGGAGAAATATCATCCACCATTACTTACGG	7912
Db	6961	CACACTCTCGACTTGATGCGATGCGCCCTTTGGAGAAATATCATCCACCATTACTTACGG	7020
QY	7913	GTACTCGTTTTAAATTCGGGGCGATGATGAATTCGGAAATGTTCTCTACACTTTTGTCA	7972
Db	7021	GTACTCGTTTTAAATTCGGGGCGATGATGAATTCGGAAATGTTCTCTACACTTTTGTCA	7080
QY	7973	ACACAGTTTGAATGTCGTATGGCCGACGACGAGACTAGAAAGCGCGCTTAAAAAGTCCA	8032
Db	7081	ACACAGTTTGAATGTCGTATGGCCGACGACGAGACTAGAAAGCGCGCTTAAAAAGTCCA	7140
QY	8033	GATGTGACGCGTTCATTGGCGACGACCAACATCATACATGAGATGATCTTGACAAAGAAA	8092
Db	7141	GATGTGACGCGTTCATTGGCGACGACCAACATCATACATGAGATGATCTTGACAAAGAAA	7200
QY	8093	TGGCTGAGAGGTGGCGCACTGGCTCAACATGGAAGTTAAGATCATGACGCACTCATCG	8152
Db	7201	TGGCTGAGAGGTGGCGCACTGGCTCAACATGGAAGTTAAGATCATGACGCACTCATCG	7260
QY	8153	GTGAGAACACACCTTAATCTTGCGGGCGGATTTATCTTGCAAGATTCGGTTACTCTCCACAG	8212
Db	7261	GTGAGAACACACCTTAATCTTGCGGGCGGATTTATCTTGCAAGATTCGGTTACTCTCCACAG	7320
QY	8213	CGTCCCGCGTGGCGGATCCCTCGTAAAAAGCGCTGTTAAGTTGGGTAAACCGCTCCACGCG	8272
Db	7321	CGTCCCGCGTGGCGGATCCCTCGTAAAAAGCGCTGTTAAGTTGGGTAAACCGCTCCACGCG	7380
QY	8273	ACGACGACCAAGACGAAACAAGAAACGCGCTCTGCTAGATGAACCAAAAGCGTGGTTTA	8332
Db	7381	ACGACGACCAAGACGAAACAAGAAACGCGCTCTGCTAGATGAACCAAAAGCGTGGTTTA	7440
QY	8333	GAGTAGGTATTAACGCGACTTTAGCAGTGGCCGGAAGACCCCGGTATGAGGTACACATA	8392
Db	7441	GAGTAGGTATTAACGCGACTTTAGCAGTGGCCGGAAGACCCCGGTATGAGGTACACATA	7500
QY	8393	TTACACCTGTCTTACTGGCAATTGGAATTTTGGCCAGACAAAAGACATTTCCAACCA	8452
Db	7501	TTACACCTGTCTTACTGGCAATTGGAATTTTGGCCAGACAAAAGACATTTCCAACCA	7560
QY	8453	TCAGAGGGGAAATTAAGCATCTCTACGGTGGTCTTAATATGTCACATAGTACATTTCAAT	8512
Db	7561	TCAGAGGGGAAATTAAGCATCTCTACGGTGGTCTTAATATGTCACATAGTACATTTCAAT	7620
QY	8513	CTGACTAATATCAACAACACACCACTT 8539	
Db	7621	CTGACTAATATCAACAACACACCACTT 7647	

RESULT	13
ABN86689	
ID	ABN86689 standard; DNA; 12110 BP.
XX	
AC	ABN86689;
XX	
DT	05-NOV-2002 (first entry)

XX Nucleotide sequence of vector Sinrep5-E7-Hep70.
DE
XX Major histocompatibility complex; MHC; antigen presenting cell; APC;
KM antigen; cytosolic; virulence; gene therapy; CD8; vaccine; therapeutic;
KM cancer; viral infection; HPV; E7; heat shock protein 70; Hep70; de.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 7715..9819
FT /tag=8
FT /note= "E7-Hep70 fusion sequence"
XX
XX MO200261113-A2.
XX
XX 06-AUG-2002.
XX
XX 01-FEB-2002; 2002WO-US002598.
XX
XX 01-FEB-2001; 2001US-0265334P.
XX
XX (UYJO) UNIV JOHNS HOPKINS.
XX
XX Wu T, Hung C;
XX
XX WPI; 2002-619261/66.
XX
XX Nucleic acid molecule encoding a fusion polypeptide that promotes
PT processing via the Major Histocompatibility Complex class I pathway
PT and/or promotes activity of an antigen presenting cell, useful as vaccine
PT for cancer and viral infections.
XX
PS Claim 36; Page 30-33; 127pp; English.
XX
XX The invention relates to a new nucleic acid molecule (I) encoding a
CC fusion polypeptide useful as a vaccine composition. (I) comprises a first
CC nucleic acid sequence encoding a first polypeptide or peptide that
CC promotes processing via the Major Histocompatibility Complex (MHC) class
CC I pathway (MHC-I-PP) and/or promotes development or activity of an
CC antigen presenting cell (APC). The second nucleic acid sequence is linked
CC in frame to the first nucleic acid sequence or to a linker nucleic acid
CC sequence and encodes an antigenic polypeptide or peptide. The methods and
CC compositions of the present invention are useful as therapeutic vaccine
CC for cancer and for major viral infections, such as hepatoma and cervical
CC cancer, that cause morbidity and mortality. They can also be used in
CC treating animal diseases, such as equine herpesvirus, bovine viruses,
CC Marek's disease, retroviral and lentiviral diseases and rabies, in the
CC veterinary medicine context. The present sequence represents the
CC nucleotide sequence of vector Sinrep5-E7-Hep70 comprising the human
CC papillomavirus (HPV) E7 antigenic protein and M. tuberculosis heat shock
CC protein 70 (Hsp70) fusion sequence
XX
XX Sequence 12110 BP; 3339 A; 3084 C; 3137 G; 2550 T; 0 U; 0 Other;
SQ
XX
XX Query March 89.4%; Score 7637.4; DB 6; Length 12110;
XX Best Local Similarity 99.9%; Pred. No. 0;
XX Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db 181 ATGCCAGAGCATTTTCCGATCTGCGCAGTAACCTAATCGAGCTGAGAGTTCTTACCAAG 240
Qy 1133 CGACGATCTTGAACATAGAGGACGACCGGCTCGTAGAATGTTTCCGAGCACCAGATATC 1192
Db 241 CGAGATCTTGAACATAGAGGACGACCGGCTCGTAGAATGTTTCCGAGCACCAGATATC 300
Qy 1193 ATTGTGTCTGCCCATATCGTATGTCAGAGAACCCGAGCCGATATGAAATAGCCAGTA 1252
Db 301 ATTGTGTCTGCCCATATCGTATGTCAGAGAACCCGAGCCGATATGAAATAGCCAGTA 360
Qy 1253 AACGCGGAGAAAAAGCGTGAAGATTACAAACAAAGCTTGATGAGAAAGTTAAGATC 1312
Db 361 AACTGCGGAAAAAGCGTGAAGATTACAAACAAAGCTTGATGAGAAAGTTAAGATC 420
Qy 1313 TCCGACCGTACTTATGATACCGCGGATGCTGTAACACCATGCTGCTTTCACACAGATG 1372
Db 421 TCCGACCGTACTTATGATACCGCGGATGCTGTAACACCATGCTGCTTTCACACAGATG 480
Qy 1373 TTACCTGCAACATGCGTCCGAATATTTCCGTATGACAGAGCTGTATATCAACGCTCCG 1432
Db 481 TTACCTGCAACATGCGTCCGAATATTTCCGTATGACAGAGCTGTATATCAACGCTCCG 540
Qy 1433 GAATATCTATCATCAGGCTATGAAAGCGTGGGAGACCTGTATCTGATGCTTTCGACA 1492
Db 541 GAATATCTATCATCAGGCTATGAAAGCGTGGGAGACCTGTATCTGATGCTTTCGACA 600
Qy 1493 CCACCGAGTTCAATGTTCCGCGCTATGGCAGGTTGCTACCGCTGACCAACCAACTGGG 1552
Db 601 CCACCGAGTTCAATGTTCCGCGCTATGGCAGGTTGCTACCGCTGACCAACCAACTGGG 660
Qy 1553 CCGAGCAAAAGTCTTGAAGCGCGTAAACATCGGACTTTGACAGCAAAAGCTGAGTAG 1612
Db 661 CCGAGCAAAAGTCTTGAAGCGCGTAAACATCGGACTTTGACAGCAAAAGCTGAGTAG 720
Qy 1613 GTAGGACAGAAAAATTTGCTGATATGAGAAAGAGGTTGAAGCCCGGCTGCGGGTTT 1672
Db 721 GTAGGACAGAAAAATTTGCTGATATGAGAAAGAGGTTGAAGCCCGGCTGCGGGTTT 780
Qy 1673 ATTTCTCGTAGAGTATGACATTTATCCAGAACACAGGCGGTGAGAGCTGGGATC 1732
Db 781 ATTTCTCGTAGAGTATGACATTTATCCAGAACACAGGCGGTGAGAGCTGGGATC 840
Qy 1733 TTCCATCGGTGTTCCATTTGATGAAAGAGTGTACCTTGGCGGTGTATACAGTGG 1792
Db 841 TTCCATCGGTGTTCCATTTGATGAAAGAGTGTATACCTTGGCGGTGTATACAGTGG 900
Qy 1793 TGAATTCGAAAGGCTAGCTAGTGAAGAAATCACCATCATAGTCCGGGATCACGGAGAA 1852
Db 901 TGAATTCGAAAGGCTAGCTAGTGAAGAAATCACCATCATAGTCCGGGATCACGGAGAA 960
Qy 1853 CCGTGGATACCGCGTTTACACAAATAGCGAGGCTTCTGTATGCAAAAGTTACTGACA 1912
Db 961 CCGTGGATACCGCGTTTACACAAATAGCGAGGCTTCTGTATGCAAAAGTTACTGACA 1020
Qy 1913 CAGTAAAGAGAAACGGGTATCGTTCCCTGTTGTCAGTACATCCGCGACCAATATGCG 1972
Db 1021 CAGTAAAGAGAAACGGGTATCGTTCCCTGTTGTCAGTACATCCGCGACCAATATGCG 1080
Qy 1973 ATCAGATGACTGTATATAGGCCACGAGATATATCATCTGACGATGACCAAAAATTCTGG 2032
Db 1081 ATCAGATGACTGTATATAGGCCACGAGATATATCATCTGACGATGACCAAAAATTCTGG 1140
Qy 2033 TTGGGCTCAACACGCAATTTGTCTTAAACGTATAGACTTAACAGAAACCAACACATGCG 2092
Db 1141 TTGGGCTCAACACGCAATTTGTCTTAAACGTATAGACTTAACAGAAACCAACACATGCG 1200
Qy 2093 AAAATTAACCTTCCGCGATCAATAGACAAAGGTTCAAGAAATGAGGCTAAGAGGCAAG 2152
Db 1201 AAAATTAACCTTCCGCGATCAATAGACAAAGGTTCAAGAAATGAGGCTAAGAGGCAAG 1260
Qy 2153 ATGATCTTGTATACGAGAAATATGCTGGGTAATAGAGAACGAACTTAAGATGAGCTGCT 2212
Db 1261 ATGATCTTGTATACGAGAAATATGCTGGGTAATAGAGAACGAACTTAAGATGAGCTGCT 1320

QY 2213 TGTGGCGTTTCGCACTAAGAAAGTACATTGTTTTATCGCCCACTGGAACGACAGACT 2272
Db 1321 TGTGGCGTTTCGCACTAAGAAAGTACATTGTTTTATCGCCCACTGGAACGACAGACT 1380
QY 2273 GCGTAAAGTCCACGCTCTTTTACGCGCTTTTCCCATGTGTGTCGTATGACACGCTCTT 2332
Db 1381 GCGTAAAGTCCACGCTCTTTTACGCGCTTTTCCCATGTGTGTCGTATGACACGCTCTT 1440
QY 2333 TGGCCATGTGCTGAGGCGAGAAATTGAACCTGGCATTCGAACCAAGAGAGAGAAAAAC 2392
Db 1441 TGGCCATGTGCTGAGGCGAGAAATTGAACCTGGCATTCGAACCAAGAGAGAGAAAAAC 1500
QY 2393 TGGTGCAGTCTCGAGAGAAATTAGTCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAGG 2452
Db 1501 TGGTGCAGGCTCGAGAGAAATTAGTCATGAGGCGCAAGGCTGCTTTTGAAGATGCTCAGG 1560
QY 2453 AGGAAGCCAGAGCGGAGAGAGCTCGAGAGACATTCACCAATTAATGTGCGACAAAGGCA 2512
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QY 2513 TCGAGGCGAGCGGAGAGTGTCTGCGAGAGTGGAGGGGCTCAAGGCGGAGCATCGAGGACG 2572
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QY 2633 TCGGACAGTATATGCTGTCTCGCCAAACTCTGTGCTGAAGAAATGCCAACTGGCACG 2692
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QY 2693 CGCACCCGCTAGAGAGATCAGATTAAATCATACACATCCGGAAGATCGAAGAGTACG 2752
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QY 2753 CGGTGCAACCATACGACGCTAAAGTACTGATGCGACAGAGAGGTGCCGTACATGCGCAG 2812
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QY 2813 AATTCTAGACCTGATGAGAGCGCCAGTTTGTATCAACGAAAGAGAGTGTGTGAACC 2872
Db 1921 AATTCTAGACCTGATGAGAGCGCCAGTTTGTATCAACGAAAGAGAGTGTGTGAACC 1980
QY 2873 GCAAACTATACCATTCGATGATGAGCGCCGCAAGAAATACAGAAAGAGAGATGACA 2932
Db 1981 GCAAACTATACCATTCGATGATGAGCGCCGCAAGAAATACAGAAAGAGAGATGACA 2040
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Db 2041 AGGTTACAAAGGAGAGCTTGCAGAAAACAGAGTACGTGTTTGAAGTGAACAGAGCGTT 2100
QY 2993 GCGTTAAGAGAGAAAGGCTCAGGTTGCTCTCTCGGAGAACTGACCAACCTCTCCT 3052
Db 2101 GCGTTAAGAGAGAAAGGCTCAGGTTGCTCTCTCGGAGAACTGACCAACCTCTCCT 2160
QY 3053 ATCATGAGTACGCTGAGAGAGAGCTGAAGACCGGACCTGCGTCCGTTACAAGGTGAAA 3112
Db 2161 ATCATGAGTACGCTGAGAGAGAGCTGAAGACCGGACCTGCGTCCGTTACAAGGTGAAA 2220
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QY 3173 CGGACGAGATCTTTGTTACAGCGGAGAAAGAAATTTGTCGAAATTTGAGCGCGACG 3232
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Db 2461 CACTACTTCCCTTGAATTTGCTATCTGTAGAGCCCGGCAAGAGATGATCTATGCGGAGACC 2520
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Db 2521 CCATGCAATGCGGATCTTCAACATGATGACAACTAAAGTATCAATTCACCTGAAA 2580
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QY 3533 CAGCTATTGTATGACACTGCACTTACGATGGAAGATGAAACCAAGAACCCCTGCAAG 3592
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QY 3653 CATGTTCCGCGGGTGGTTAAGCAATTGCAATTCGATTCGCGACATGAAGTATGA 3712
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Db 2821 CAGCCCGGCTTCAACAAGGCTTACCAAGAAAGAGATGATGCGGCTCCGCAAAAAGTCA 2880
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QY 3953 TTGCTCAATTAACACGCCCACTCCCGTGCCAATCCGTTCAAGCTCAAGACCAACGTTT 4012
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Db 3121 GCTGGCGAAAGCATTTGAAACCGATATCTAGCCACGGCCGGTATGTTACCGGTTGCC 3180
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QY 4133 TAGACGTAATTTGCAATTAAGTTTTCGGCATGAGACTTGAACAAGCGGACTTTTCTAAC 4192
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QY 4193 AGAGCATCCCACTAACGTAACATCCCGCGATTCAGCGAGGCCGGTATGCTCATTTGGGACA 4252
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QY 4253 ACAGGCCAGAAACCCGCAAGTATGGTATGATACGCCCATTTGCCCGCAACTCTCCCGTA 4312
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QY 4313 GATTTCCGGTTCAGAGTACGAGGAGGACCAACCTTGAATTTGACAGACGGGAGAA 4372
Db 3421 GATTTCCGGTTCAGAGTACGAGGAGGACCAACCTTGAATTTGACAGACGGGAGAA 3480
QY 4373 CCAGAGTATCTGTGACAGCATTAACCTGTCGCGGTGAACCGCAATCTTCTCAACGCT 4432

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Db 3541 TAGTCCCGAGTACAGAGAGAGCAACCGGCGCGGTCAAAAAATTCCTGAAACAGTTCA 3600
Qy 4493 AACACCACTAGTACTTGTGTATCAGAGGAAAAATTTGAAGCTCCCGTAAAGAAATCG 4552
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Qy 4553 AATGGATCGCCCGATTTGGCATAGCCGGTGCATTAAGAACTAACACTGGCTTTGGGT 4612
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Db 3781 ACCACTTTCAAGCATGTCGAGAACCATGCGGCACTTAAAAACCTTTTCGGGTTCGCGCC 3840
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Db 3901 ACAGTGAAGCATGTGATACCGGCTTGTCCAGAAATTTGTCAAGGATGTCTGCAACGAGAC 3960
Qy 4853 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGAACTAGACAACAGACC 4912
Db 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGAACTAGACAACAGACC 4020
Qy 4913 GTACACGGCAATTCACCCCGCACTGAAATTCGTGATTTTCGTCCGTGTATGAGGTA 4972
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Qy 5033 GTCAAGAGAAAGAGTGTCAACGACCAATTCGCTGGTGAACAGGCGAAGAGTCT 5092
Db 4141 GTCAAGAGAAAGAGTGTCAACGACCAATTCGCTGGTGAACAGGCGAAGAGTCT 4200
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Db 4261 CCGCAAAATGATCTGTGCTAGAAAAGAAAGTATCCAGCGGTGGCCCTGATTTCC 4320
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Qy 5393 GAATGACGCGAGAGTAAACATCTATTGCTGATTAAGAGTGAAGAGAAAGAAATCGAG 5452
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Db 5221 GCTCACTTTTTCAGCTTTAGCGGATTCGACCACTATTTACTATTAAGAGAGTGGT 5280
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Db 5281 CGTCAGAGCTTAATTCATAGATAGTAAACGAGAGAGAGTGTGTGCTGACGTTTC 5340
Qy 6233 ATGCGGTCCAAAGACCTGCGCTTATTCACCGGCAAGGCTTAAAGATGGCCCGGCTGG 6292
Db 5341 ATGCGGTCCAAAGACCTGCGCTTATTCACCGGCAAGGCTTAAAGATGGCCCGGCTGG 5400
Qy 6293 CAGCGGAAGAAAGAGAGCCCACTCAACGCGCAACAAATAGCTGAGTCCCTCCACCTCT 6352
Db 5401 CAGCGGAAGAAAGAGAGCCCACTCAACGCGCAACAAATAGCTGAGTCCCTCCACCTCT 5460
Qy 6353 CTTTGTGTGGGTATTCATGATCCCTGAGATCAATTTTTCAGAGAGAGAGCGCCGCAAG 6412
Db 5461 CTTTGTGTGGGTATTCATGATCCCTGAGATCAATTTTTCAGAGAGAGAGCGCCGCAAG 5520
Qy 6413 CAGCGGTAAACCCCTGAGCAACAGGCGGCAACGAGTGTGCTATGCTTTTGGATCGTTT 6472
Db 5521 CAGCGGTAAACCCCTGAGCAACAGGCGGCAACGAGTGTGCTATGCTTTTGGATCGTTT 5580
Qy 6473 CCGAGAGAGATTAAGTGAAGCTGAGCGGAGAGTAACTGAGTCCGAAACCCGCTCTGTTTG 6532
Db 5581 CCGAGAGAGATTAAGTGAAGCTGAGCGGAGAGTAACTGAGTCCGAAACCCGCTCTGTTTG 5640
Qy 6533 GATCATTTGAAACCGGCGAAGTGAACCTCAATTAATATATGCTCCGATCAGCCGATCTTTC 6592
Db 5641 GATCATTTGAAACCGGCGAAGTGAACCTCAATTAATATATGCTCCGATCAGCCGATCTTTC 5700
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[illegible]

OY	7673	TTCCAAACATTCAACGCTTTTGGACATGTCGGCGGAGATTTTGGATCAATATACAG	7732
Db	6781	TTCCAAACATTCAACGCTTTTGGACATGTCGGCGGAGATTTTGGATCAATATACAG	6840
OY	7733	AAACAATTCAAGCAAGCGGACCCGGTACTGGAGACGGATATCGCATCTTTGACAAAGCC	7792
Db	6841	AAACAATTCAAGCAAGCGGACCCGGTACTGGAGACGGATATCGCATCTTTGACAAAGCC	6900
OY	7793	AAGACGACGCTATAGCGGTTAAACGGGTGTGATGATCTTGGAGGACCTGGGTTGGATCAAC	7852
Db	6901	AAGACGACGCTATAGCGGTTAAACGGGTGTGATGATCTTGGAGGACCTGGGTTGGATCAAC	6960
OY	7853	CACACTCGACTGATGATGAGTGGCGCTTTGGAGAAATATCATCCACCATCTACCTACGG	7912
Db	6961	CACACTCGACTGATGATGAGTGGCGCTTTGGAGAAATATCATCCACCATCTACCTACGG	7020
OY	7913	GTACTCGTTTAAATTCGGGGCGCATGATGAAATCCGGAAATGTTCTCCACCTTTTGTCA	7972
Db	7021	GTACTCGTTTAAATTCGGGGCGCATGATGAAATCCGGAAATGTTCTCCACCTTTTGTGCA	7080
OY	7973	ACACAGTTTGAATGTGCTTATCGCCACAGAGTACTAGAAAGCGGCTTTAAACGTCCA	8032
Db	7081	ACACAGTTTGAATGTGCTTATCGCCACAGAGTACTAGAAAGCGGCTTTAAACGTCCA	7140
OY	8033	GATGTGCAGCGTTTCATTGGCGACGACAACATCATACATGAGATGATCTTGACAAAGAA	8092
Db	7141	GATGTGCAGCGTTTCATTGGCGACGACAACATCATACATGAGATGATCTTGACAAAGAA	7200
OY	8093	TGGCTGAGAGGTGGCGCACCTGGGTTCAACATGAGAGTTAAGATCATCGACGCACTCATCG	8152
Db	7201	TGGCTGAGAGGTGGCGCACCTGGGTTCAACATGAGAGTTAAGATCATCGACGCACTCATCG	7260
OY	8153	GTGAGAGACCACTTACTTCTGCGGCGGATTTATCTTGACAATTCGTTACTTCCACAG	8212
Db	7261	GTGAGAGACCACTTACTTCTGCGGCGGATTTATCTTGACAATTCGTTACTTCCACAG	7320
OY	8213	CGTCCCGCGTGGCGGATTCCTCTGAAAAGGCGTTTAGTTGGGTTAAACCGCTCCACAGCG	8272
Db	7321	CGTCCCGCGTGGCGGATTCCTCTGAAAAGGCGTTTAGTTGGGTTAAACCGCTCCACAGCG	7380
OY	8273	ACGACGAGCAAGACGAGAGACAGAAAGCGCGTCTGTAGATGAAACAAAGGCGTGTTTA	8332
Db	7381	ACGACGAGCAAGACGAGAGACAGAAAGCGCGCTGTAGATGAAACAAAGGCGTGTTTA	7440
OY	8333	GAGTAGGTATTAACGCGCACTTTAGCACTGGCCGTGACGACCCCGGTATGAGTTAGACATA	8392
Db	7441	GAGTAGGTATTAACGCGCACTTTAGCACTGGCCGTGACGACCCCGGTATGAGTTAGACATA	7500
OY	8393	TTTACACCTGTCTACTGSCATTTGAGAACTTTTGCCACGAGCAAAAGACATTTCCAAAGCA	8452
Db	7501	TTTACACCTGTCTACTGSCATTTGAGAACTTTTGCCACGAGCAAAAGACATTTCCAAAGCA	7560
OY	8453	TCAGAGGGGAAATTAAGCATCTCTACGCTGTCTTAATATGTCAGCATAGTACATTTTCAT	8512
Db	7561	TCAGAGGGGAAATTAAGCATCTCTACGCTGTCTTAATATGTCAGCATAGTACATTTTCAT	7620
OY	8513	CTGACTAATACTACAAACCAACCACT 8539	
Db	7621	CTGACTAATACTACAAACCAACCACT 7647	

RESULT 14

ID AAX77358 standard; DNA; 13905 BP.

AC AAX773587

DT 09-AUG-1999 (first entry)

Polynucleotide sequence of pT5'23

KW Nucleic acid identification; exogenous protein; gene sorting
growth factor; membrane receptor; simblis virus; ss.

XX OS Synthetic.
XX PN MO9925876-A1.
XX PD 27-MAY-1999.
XX PF 17-NOV-1998; 98WO-US024520.
XX PR 17-NOV-1997; 97US-00972218.
XX PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.
PI Bailey JE, Renner WA, Orberger GH, Koller D;
XX WP1; 1999-357620/30.
XX PT Isolating genes encoding proteins with selected properties, useful for
XX identifying therapeutic agents or targets.
PS Disclosure; Fig 12A-D; 136pp; English.
XX CC The invention relates to the identification of a recombinant nucleic acid
XX encoding an exogenous protein having a selected property. The method
XX comprises preparing a population of eukaryotic host cells, culturing the
XX cells under suitable conditions and identifying cells that contain the
XX recombinant nucleic acid. The method is used to sort genes according to
XX the type of proteins they express, and also to identify new ligand/
XX receptor interactions. Typical applications of the nucleic acid and the
XX exogenous protein are in isolation of new growth factors, cytokines,
XX membrane receptors, cytoplasmic, organelle or nuclear proteins, all of
XX which may be useful as therapeutic agents or therapeutic targets, e.g.
XX apoptosis-promoting or tumour suppressing proteins, regulators of cell
XX proliferation or metabolic processes etc. The protein can also be used to
XX screen for specific modulators. The nucleic acid can also be used as
XX sources of therapeutic antisense or ribozyme sequences. The method allows
XX the protein (rather than a partial DNA sequence) to be isolated and,
XX since a wide range of cells can be used, they can be expressed with the
XX correct glycosylation pattern.
SQ Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;
Query Match 89.4%; Score 7637.4; DB 2; Length 13905;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 893 ATTGACGGCGGTAGTACACACTATTGAATCAAAAGCCGACCAATTGCACTACATCAAA 952
DB 1 ATTGACGGCGGTAGTACACACTATTGAATCAAAAGCCGACCAATTGCACTACATCAAA 60
QY 953 TGGAGAACCGAGTAGTAAGTAGACGAGCCCGAGTCCGTTTGTGCTGCACTGC 1012
DB 61 TGGAGAACCGAGTAGTAAGTAGACGAGCCCGAGTCCGTTTGTGCTGCACTGC 120
QY 1013 AAAAAAAGCTTCCCGCAATTTAGAGTAGTACAGACAGAGTCACTCAAAATGACCATGCTA 1072
DB 121 AAAAAAAGCTTCCCGCAATTTAGAGTAGTACAGACAGAGTCACTCAAAATGACCATGCTA 180
QY 1073 ATGCGAAGCATTTTCCGATCTGCGCCAGTAATCTAATGAGCTGAGAGTTCTTACCAAG 1132
DB 181 ATGCGAAGCATTTTCCGATCTGCGCCAGTAATCTAATGAGCTGAGAGTTCTTACCAAG 240
QY 1133 CGAGCATCTTGGATAGGAGCGGACCGGCTGCTAGAAATGTTTCCGAGAGACAGATATC 1192
DB 241 CGAGCATCTTGGATAGGAGCGGACCGGCTGCTAGAAATGTTTCCGAGAGACAGATATC 300
QY 1193 ATTGTGTCTGCCCATGCGTGTAGTCCAGAGAGACCGGACCGCATGATGAATACCCAGTA 1252
DB 301 ATTGTGTCTGCCCATGCGTGTAGTCCAGAGAGACCGGACCGCATGATGAATACCCAGTA 360
QY 1253 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAAGAACTTGATGAGAGATTAAAGATC 1312
DB 361 AACTGGCGGAAAAAGCGTGCAAGATTACAAACAAAGAACTTGATGAGAGATTAAAGATC 420

QY 1313 TCCGAGACCGTACTTGATACGCGGATGCTGTAAACACCATGCTGTCTTTCACAAAGATG 1372
DB 421 TCCGAGACCGTACTTGATACGCGGATGCTGTAAACACCATGCTGTCTTTCACAAAGATG 480
QY 1373 TTACCTGCAACATCGGCGCCGAATATTTCCGTATGACGAGACGTGTATATCAACCTCCCG 1432
DB 481 TTACCTGCAACATCGGCGCCGAATATTTCCGTATGACGAGACGTGTATATCAACCTCCCG 540
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DB 541 GAATCTATCTATCATCAGAGCTATGAAGAGCGGACCGGTGATCTGATTTGGCTTCGACA 600
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DB 721 GTAGAGAGGAAATTTGTGATATAGAGAAAGAGTGAAGCCGGGTGCGGGGTTT 780
QY 1673 ATTTCCTCGTAGATTCGACACTTTATCCAGAACACAGAGCAGCTTGACAGCTGGCATC 1732
DB 781 ATTTCCTCGTAGATTCGACACTTTATCCAGAACACAGAGCAGCTTGACAGCTGGCATC 840
QY 1733 TTCCATGCTGTTCACCTTGATGAAGAGAGCTGTACCTTGGCTGTGTATCACTGG 1792
DB 841 TTCCATGCTGTTCACCTTGATGAAGAGAGCTGTACCTTGGCTGTGTATCACTGG 900
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DB 901 TGAATTCGAAAGGTAGTGTAGTAAGAAATACACATCAGTCCGGGATACCGGAGAA 960
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DB 1021 CAGTAAAGAGAAAGGATATCGTTCCTGTGTGACAGTACATCCGGGACCATATGCG 1080
QY 1973 ATCAGATGATCTGTATATATGCGCACGATATATCACTGACGATGCAAAAACCTTCTGG 2032
DB 1081 ATCAGATGATCTGTATATATGCGCACGATATATCACTGACGATGCAAAAACCTTCTGG 1140
QY 2033 TTGGGCTCAACAGCAATGTGCTATTAACGGTAGACCTAACAGAAACCAACACATATG 2092
DB 1141 TTGGGCTCAACAGCAATGTGCTATTAACGGTAGACCTAACAGAAACCAACACATATG 1200
QY 2093 AAAAAAAGCTTCCCGCAATTTAGAGTAGTACAGACAGAGTCACTCAAAATGACCATGCTA 2152
DB 1201 AAAAAAAGCTTCCCGCAATTTAGAGTAGTACAGACAGAGTCACTCAAAATGACCATGCTA 1260
QY 2153 ATGATCTTGTATACGAGAAATGCTGGGTACTAGAGAACGACCTTACGATATGCTGCT 2212
DB 1261 ATGATCTTGTATACGAGAAATGCTGGGTACTAGAGAACGACCTTACGATATGCTGCT 1320
QY 2213 TGTGGGGGTTTCCGACTAAGAAAGTACATTCGTTTATGCGCCACCTGGAACGAGACCT 2272
DB 1321 TGTGGGGGTTTCCGACTAAGAAAGTACATTCGTTTATGCGCCACCTGGAACGAGACCT 1380
QY 2273 GCGTAAAGTCCAGCCTCTTTTAAAGCCTTTTCCCATGTCGTCCGTATGAGAGACCTCTT 2332
DB 1381 GCGTAAAGTCCAGCCTCTTTTAAAGCCTTTTCCCATGTCGTCCGTATGAGAGACCTCTT 1440
QY 2333 TGCCCATGTGCTGAGGACAGAAATTTGAACCTGGCATTTGCAACCAAGAGAGGAAAAAC 2392
DB 1441 TGCCCATGTGCTGAGGACAGAAATTTGAACCTGGCATTTGCAACCAAGAGAGGAAAAAC 1500

QY 2393 TGCTGACGCTCTCGAGGAATTAATCATGAGGCCAAGGCTGCTTTTGAAGATGCTCAGG 2452
Db 1501 TGCTGACGCTCTCGAGGAATTAATCATGAGGCCAAGGCTGCTTTTGAAGATGCTCAGG 1560
QY 2453 AGGAAGCCAGAGCGGAGAACTCCGAGAACACTTCCACATTAATAGTGGCAGACAAAGGCA 2512
Db 1561 AGGAAGCCAGAGCGGAGAACTCCGAGAACACTTCCACATTAATAGTGGCAGACAAAGGCA 1620
QY 2513 TCGAGGACGCGGAGAAAGTTGCTGCGAATGAGGGGCTCCAGGCGGACATCGAGCAG 2572
Db 1621 TCGAGGACGCGGAGAAAGTTGCTGCGAATGAGGGGCTCCAGGCGGACATCGAGCAG 1680
QY 2573 CATTAGTTGAAACCCCGCGGCTCAGTAAGATTAATCTCAAGCAATAGACCGTATGA 2632
Db 1681 CATTAGTTGAAACCCCGCGGCTCAGTAAGATTAATCTCAAGCAATAGACCGTATGA 1740
QY 2633 TCGGACAGTATTCGTTGTCTCCGCAACCTGTGTGTAAGAAATGCCAACTGGCAGCAG 2692
Db 1741 TCGGACAGTATTCGTTGTCTCCGCAACCTGTGTGTAAGAAATGCCAACTGGCAGCAG 1800
QY 2693 CGCACCCGCTAGCAGATCAGATTAAATCAACACTCCGGAAGATCAGAAAGTACG 2752
Db 1801 CGCACCCGCTAGCAGATCAGATTAAATCAACACTCCGGAAGATCAGAAAGTACG 1860
QY 2753 CGGTCGAACCATAGCAGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGGCAG 2812
Db 1861 CGGTCGAACCATAGCAGCTAAAGTACTGATGCCAGAGAGGTGCCGTACCATGGCAG 1920
QY 2813 AATTCCTAGACCTGAGTGAAGAGCGCCAGTTAGTGTCAACGAAAGAAATTTGTGAAC 2872
Db 1921 AATTCCTAGACCTGAGTGAAGAGCGCCAGTTAGTGTCAACGAAAGAAATTTGTGAAC 1980
QY 2873 GCAAACTATACCACTTGCCATGCTGCCCCCGCAAGATATACGAAGAGAGCAGTACA 2932
Db 1981 GCAAACTATACCACTTGCCATGCTGCCCCCGCAAGATATACGAAGAGAGCAGTACA 2040
QY 2933 AGGTTCAAAAGGAGAGCTTGACAGAAACAGAGTACGTGTTGACGTGGACAAAGAGCTT 2992
Db 2041 AGGTTCAAAAGGAGAGCTTGACAGAAACAGAGTACGTGTTGACGTGGACAAAGAGCTT 2100
QY 2993 GCGTTAAGAAAGAAAGCCTCAAGTCTGCTCTGGGAGAACTGACCAACCTCCCT 3052
Db 2101 GCGTTAAGAAAGAAAGCCTCAAGTCTGCTCTGGGAGAACTGACCAACCTCCCT 2160
QY 3053 ATCATGAGTACGCTGAGAGGAGCTGAAAGACCCGACCTGCGGTCCGTTACAAAGTCCGAAA 3112
Db 2161 ATCATGAGTACGCTGAGAGGAGCTGAAAGACCCGACCTGCGGTCCGTTACAAAGTCCGAAA 2220
QY 3113 CAATAGAGTATAGGACACCGGGGTGCGGCAAGTCAAGCTATTAAGTCAACTGTCA 3172
Db 2221 CAATAGAGTATAGGACACCGGGGTGCGGCAAGTCAAGCTATTAAGTCAACTGTCA 2280
QY 3173 CGGACAGAGATCTTGTTACAGCGGGAAGAAATTTGCGGAATTTGAGGCGGACG 3232
Db 2281 CGGACAGAGATCTTGTTACAGCGGGAAGAAATTTGCGGAATTTGAGGCGGACG 2340
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Db 2401 GATGCCACAAAGCCGTAGAAAGTGTGTAAGTGAAGAGGCTTCCGTCACGCAAGAG 2460
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Db 2461 CACTACTTGCTTGATGATGCTATGCTCAGGCCCCGCAAGAAAGTATGTAAGCGAACC 2520
QY 3413 CCATGCAATGCGGATTTCTTCAACATGATGCACTAAAGATCAATTTCAATCAACCTGAAA 3472
Db 2521 CCATGCAATGCGGATTTCTTCAACATGATGCACTAAAGATCAATTTCAATCAACCTGAAA 2580
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Db 2581 AAGACATATGCAACCAAGACATTTCTAACAGTATATCTCCCGCGTTGACACAGCCAGTTA 2640
QY 3533 CAGCTATTGATGCACTGCACTTAATGATGAGAAAGTGAACACAGAAACCCGTGCAGA 3592
Db 2641 CAGCTATTGATGCACTGCACTTAATGATGAGAAAGTGAACACAGAAACCCGTGCAGA 2700
QY 3593 AGAACATTGAAATTCATATTAAGAGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGA 3652
Db 2701 AGAACATTGAAATTCATATTAAGAGGGCCACAAAGCCGAAGCCAGGGGATATCATCTGA 2760
QY 3653 CATGTTTCCGGGGGTGGTTAAGCAATTGCAATTCATATCCCGGACATGAAGTAAATGA 3712
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Db 2821 CAGCGCGGCTCACAAGAGGCTAACAGAAAAGAGTATGCGCTCCGCAAAAAGTCA 2880
QY 3773 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTCTCACCCGACTG 3832
Db 2881 ATGAAAACCCACTGTACGCGATCACATCAGAGCATGTGAACGTGTCTCACCCGACTG 2940
QY 3833 AGGACAGGCTAGTGTGAAAACCTTGACAGGCGACCCATGATTAAGACGCCACTAAC 3892
Db 2941 AGGACAGGCTAGTGTGAAAACCTTGACAGGCGACCCATGATTAAGACGCCACTAAC 3000
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Db 3001 TACCTAAGAAAACCTTCAGGCTATATAGAGGACTGAGAAAGCTGAAACAAAGGAATAA 3060
QY 3953 TTGCTCAATTAACAGCCCACTCCCGTGCATTCGTTCACTGACCTGCAAGACCAACGTTT 4012
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QY 4013 GCTGGCGAAAGATTTGGAACCGATCTAGCCACGCGCGGTATCTGATCCGGTTGCC 4072
Db 3121 GCTGGCGAAAGATTTGGAACCGATCTAGCCACGCGCGGTATCTGATCCGGTTGCC 3180
QY 4073 AGTGAAGCAACCTGTTCCCAAGTTGGAGTATGACAAACCAATTCGGCATTTACGCT 4132
Db 3181 AGTGAAGCAACCTGTTCCCAAGTTGGAGTATGACAAACCAATTCGGCATTTACGCT 3240
QY 4133 TAGACGTAATTTGTCATTAAGTTTTCGGACATGAGCTTGAACAGCGGACTGTTTCTAAC 4192
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QY 4253 ACAGCCCAAGAAACCCCAAGTATGGTATGATCAGATCAGCCATTGCGCGCAACTCTCCGTA 4312
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QY 4313 GATTTCCGTTGTTCCAGTACGTTAGGGAAGGGCACACAACTTGATTGACAGCGGGAGAA 4372
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QY 4373 CCAAGTATCTTGTGACAGCATTAACCTGTTCCCGGTGAACCGGCATCTTCCACGCGCT 4432
Db 3481 CCAAGTATCTTGTGACAGCATTAACCTGTTCCCGGTGAACCGGCATCTTCCACGCGCT 3540
QY 4433 TAGTCCCGAGTACAGAGAAACCAACCGGCGCGGTCAAAAATTTCTTGAACAGTTCA 4492
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QY 4553 AATGATCGCCCGATTTGGCATAGCCGGTGCAGATTAAGAACTAACCTGGCTTCCGGT 4612

Dh 3661 AATGATGCCCGGATTTGGCATCCGGTGCATTAAGAACTACACCTGGCTTTCCGGT 3720
Qy 4613 TTCCGCGCAGGACGGTAGCACTGGTGTTCATCAATTTGGAATTAATACAGAAACC 4672
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Dh 3781 ACCACTTTACAGCACTGGGAAGACCATGGCGGACCTTAAAAACCTTTCCGGTTCGGCCC 3840
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Dh 3841 TGAATTTTAACTCAGAGAGGACCCCTGGTGAAGTCTTAAGGCTAGCGCGACCGCA 3900
Qy 4793 ACAGTAGAGACGTAGTACACGCTCTTCCAGAAAGTTGTCAAGGCTTCTGCAGCGAGAC 4852
Dh 3901 ACAGTAGAGACGTAGTACACGCTCTTCCAGAAAGTTGTCAAGGCTTCTGCAGCGAGAC 3960
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Dh 3961 CAGATTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGACAACTAGACAAACGCC 4020
Qy 4913 GTACACGGCAATTAACCCCGACATCTGAATTTGGCTGATTTTCCGCTGTATAGAGGTA 4972
Dh 4021 GTACACGGCAATTAACCCCGACATCTGAATTTGGCTGATTTTCCGCTGTATAGAGGTA 4080
Qy 4973 CAAGAGATGAGTGGAGCGCGCGCTCATPACCGCACCAAAAGGAGAAATTTCTGACT 5032
Dh 4081 CAAGAGATGAGTGGAGCGCGCGCTCATPACCGCACCAAAAGGAGAAATTTCTGACT 4140
Qy 5033 GTCAAGAGAGACGATTGTCAACGACGCCAATCCGCTGGGTAGACAGCGGAGAGAGTCT 5092
Dh 4141 GTCAAGAGAGACGATTGTCAACGACGCCAATCCGCTGGGTAGACAGCGGAGAGAGTCT 4200
Qy 5093 GCCGTGCATCTATTAACGTTTGGCGGACAGTTTACCGATTTACCGACCAAGGAGACAGCA 5152
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Qy 5153 CCGCAAAATGACTGTGTGCTAGAAAGAAAGTATCCAGCGCGGTGGCGCTGATTTCC 5212
Dh 4261 CCGCAAAATGACTGTGTGCTAGAAAGAAAGTATCCAGCGCGGTGGCGCTGATTTCC 4320
Qy 5213 GGAAGACCCAGAGACGAAAGCTTGAATTTGCTAACAAAGCCTACATGCACTGGCAG 5272
Dh 4321 GGAAGACCCAGAGACGAAAGCTTGAATTTGCTAACAAAGCCTACATGCACTGGCAG 4380
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Qy 5453 CCGCACTTCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGATGAAGATTCAGCAG 5512
Dh 4561 CCGCACTTCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGATGAAGATTCAGCAG 4620
Qy 5513 ATGAGTTAGTATGATTCATCGACAGTGTCTGAAGGGAAGAAAGGATTCAGTACTA 5572
Dh 4621 ATGAGTTAGTATGATTCATCGACAGTGTCTGAAGGGAAGAAAGGATTCAGTACTA 4680
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Dh 4921 TCCACAGACTTAGAAGCAATTAAGTCAAGAAAGTAAAGTATGATGCTCCACCCCTTC 4980
Qy 5873 CTAGACCAAAATTAAGAAATGTTCAAGAGTTCAAGTCAAGAAAGTATGCTCTTTAATC 5932
Dh 4981 CTAGACCAAAATTAAGAAATGTTCAAGAGTTCAAGTCAAGAAAGTATGCTCTTTAATC 5040
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Qy 5993 CTCTCTCTGACAGGCGGAGAGGCGCCGGAAGTTGTAAGGACACCGTCACTTACAG 6052
Dh 5101 CTCTCTCTGACAGGCGGAGAGGCGCCGGAAGTTGTAAGGACACCGTCACTTACAG 5160
Qy 6053 CTGATTAACACTCGCTTATGATGTCACAGACATCTCACTGATTAATGATGACAGTACGAG 6112
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Dh 5281 CGTCAGGACCTAGTCACTAGAGTAGTAGACCGAAGCGAGTGTGTGTGACGTTTC 5340
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Dh 5401 CAGCGCAAGAAAGAGCCCACTTCACCGGCAAGCAATAGCTGTAGTCCCTCCACTCT 5460
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Dh 5461 CTTTGTGTGGGTATCCATGTCCTCGGATCAATTTTTCAGACGAGAACCGCCCGCCAGG 5520
Qy 6413 CAGCGTACAAACCCCTGGCAACAGGCCCCACGAGTGTGCTATGTCTTTGCGATCGTTT 6472
Dh 5521 CAGCGTACAAACCCCTGGCAACAGGCCCCACGAGTGTGCTATGTCTTTGCGATCGTTT 5580
Qy 6473 CCGACGAGAGATTTAGTATGAGCTGAGCGGACAGATTAAGTGAATCCGCTCTGTTTG 6532
Dh 5581 CCGACGAGAGATTTAGTATGAGCTGAGCGGACAGATTAAGTGAATCCGCTCTGTTTG 5640
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Db 5941 AAGCCAAACAAGATAGGTACAGTCTCGTAAGATAGAAATCAGAAAGCCATAACCACTG 6000
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Qy 7073 ATCAGATTACTGACGAGTACGATGCTTATGATATGATGAGACGAGCAGTCCATGCC 7132
Db 6181 ATCAGATTACTGACGAGTACGATGCTTATGATATGATGAGACGAGCAGTCCATGCC 6240
Qy 7133 TGGATATCTGCAACTCTTGCCCGGCTAAAGCTTGAAGTTACCCGAAAAACATGAGTATA 7192
Db 6241 TGGATATCTGCAACTCTTGCCCGGCTAAAGCTTGAAGTTACCCGAAAAACATGAGTATA 6300
Qy 7193 GAGCCCGGAATATCCGAGTGCAGTTCATCAGGAGTGCAGAACGCTCAAAATGTGC 7252
Db 6301 GAGCCCGGAATATCCGAGTGCAGTTCATCAGGAGTGCAGAACGCTCAAAATGTGC 6360
Qy 7253 TCATTGCGCGAACTTAAAGAAATTTGCAACGTCAACGAGATGCGTGAACCTGCCAACACTG 7312
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Db 6901 AAGACGAGCTATGAGCGTTAAACCGATCTGATGATCTTGAAGAGACTGAGGATGATCAAC 6960
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Db 6961 CACTACTGACTTATGATGAGTGCCTTTGGAAGAAATATCATCAACCATCTACTACCGG 7020
Qy 7913 GTACTCGTTTAAATTCGGGGGATGATGAAATCCGGAATGTTCTCACACTTTTGTCA 7972
Db 7021 GTACTCGTTTAAATTCGGGGGATGATGAAATCCGGAATGTTCTCACACTTTTGTCA 7080
Qy 7973 ACAAGTTTGAATGTCGTTATTCGCCAGCAGAGTACTAGAAAGCGGCTTAAACGTCCA 8032
Db 7081 ACAAGTTTGAATGTCGTTATTCGCCAGCAGAGTACTAGAAAGCGGCTTAAACGTCCA 7140
Qy 8033 GATGTCAGCGTTCATTTGGCGACGACCAATATCATGAGATGATGATGACAAAGAA 8092
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Qy 8093 TGGCTGAGAGGTGCGCCACTGCTCAACATGAGAGTTAAGATCATCGACGATCATCG 8152
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Qy 8153 GTGAGAGACCACTTACTTCTGCGGCGGATTTATCTTGCAAGATTTGGTTACTTCCACAG 8212
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Qy 8393 TTACACTGTCCTACCTGAGGATTTGAGAACTTTGGCCAGAGCAAAAGGATTTCCAGGCCA 8452
Db 7501 TTACACTGTCCTACCTGAGGATTTGAGAACTTTGGCCAGAGCAAAAGGATTTCCAGGCCA 7560
Qy 8453 TCAGAGGGGAAATTAAGACATCTCTACGATGCTCTAAATAGTCAAGATAGTACATTTCA 8512
Db 7561 TCAGAGGGGAAATTAAGACATCTCTACGATGCTCTAAATAGTCAAGATAGTACATTTCA 7620
Qy 8513 CTGACTAATATCTACCAACCAACCACTT 8539
Db 7621 CTGACTAATATCTACCAACCAACCACTT 7647

RESULT 15
AAA90390 standard; DNA; 13905 BP.
XX
AC AAA90390;
XX
DT 10-JAN-2001 (first entry)
XX
XX Plasmid pTBS'2J DNA sequence.
DE
XX Nucleic acid identification; exogenous protein; drug screening;
KW recombinant expression; pTBS'2J; cyclic; circular; ds.
XX
OS Synthetic.
XX
PN JP2000189173-A.
XX
PD 11-JUL-2000.
XX
XX 23-AUG-1999; 99JP-00236220.
XX
XX 17-NOV-1998; 98US-00193707.
PR 17-NOV-1998; 98WO-US024520.
XX
PA (CYTO-) CYTOS BIOTECHNOLOGY GMBH.

XX WPI: 2000-551637/51.
 XX Identifying a recombinant nucleic acid to identify and isolate various
 PT cellular proteins, comprises culturing a composition comprising
 PT eukaryotic host cells and identifying a cell comprising recombinant
 PT nucleic acid.

XX Example; Fig 12A-D; 56pp; Japanese.

XX The invention relates to the identification of a recombinant nucleic acid
 CC encoding an exogenous protein having a selected property. The method
 CC comprises preparing populations of eukaryotic host cells, where each cell
 CC comprises an expression vector encoding a different exogenous protein.
 CC The host cells are cultured under suitable conditions and the nucleic
 CC acid which encodes the exogenous protein is identified. The method is
 CC useful for the identification and isolation of proteins with a selected
 CC property. Typical applications of the nucleic acid and the exogenous
 CC protein are in isolation of new growth factors, cytokines, membrane
 CC receptors, cytoplasmic, organelle or nuclear proteins, all of which may
 CC be useful as therapeutic agents or therapeutic targets, e.g., pro-
 CC apoptotic or tumour suppressing proteins, regulators of cell
 CC proliferation or of metabolic processes. The protein can also be used to
 CC screen for ligands and specific modulators of activity. The method of the
 CC invention allows the direct cloning of full length cDNAs in one step. It
 CC facilitates direct expression of the protein without the need to perform
 CC further procedures such as subcloning and establishment of a cell line
 CC for protein production. The method allows a protein of interest (rather
 CC than a partial DNA sequence) to be isolated and, since a wide range of
 CC cell types can be used, they can be expressed in a correctly folded and
 CC glycosylated form. The present sequence represents plasmid pBS-20 which
 CC was used in the exemplifications of the invention. This patent is related
 CC to WO925876

SO Sequence 13905 BP; 3931 A; 3551 C; 3440 G; 2983 T; 0 U; 0 Other;

Query Match 89.4%; Score 7637.4; DB 3; Length 13905;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 7641; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 893 ATTAGCGGCGTAGACACATTTGAATCAACAGCCGCAATTTGCACTTCACTCA 952
 DB 1 ATTACCGCGTAGACACATTTGAATCAACAGCCGCAATTTGCACTTCACTCA 60
 QY 953 TGGAGAACCCAGTAGTAAACGTAGACGACCCCGAGTCCGTTTGTCTGCACTGC 1012
 DB 61 TGGAGAACCCAGTAGTAAACGTAGACGACCCCGAGTCCGTTTGTCTGCACTGC 120
 QY 1013 AAAAAGCTTCCGCAATTTGAGGTAGTACAGACAGAGTCACTCAATAGCAGTGA 1072
 DB 121 AAAAAGCTTCCGCAATTTGAGGTAGTACAGACAGAGTCACTCAATAGCAGTGA 180
 QY 1073 ATGCGAAGCATTTTTCGATCTGGCCAGTAACTTAATGAGCTGAGGTTCTTACACAG 1132
 DB 181 ATGCGAAGCATTTTTCGATCTGGCCAGTAACTTAATGAGCTGAGGTTCTTACACAG 240
 QY 1133 CGACGATCTTGGACATAGGACGACGACCGGCTCGTAGAATGTTTTCCGAGACCAAGTATC 1192
 DB 241 CGACGATCTTGGACATAGGACGACGACCGGCTCGTAGAATGTTTTCCGAGACCAAGTATC 300
 QY 1193 ATTTGTCTGCGCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATATACCCAGTA 1252
 DB 301 ATTTGTCTGCGCCATGCGTAGTCCAGAAAGACCCGACCGCATGATGAATATACCCAGTA 360
 QY 1253 AACTGCGGAAAAAGCGTGCAGATTTACAAAGAACTTTCATGAGAAAGTTAAGATC 1312
 DB 361 AACTGCGGAAAAAGCGTGCAGATTTACAAAGAACTTTCATGAGAAAGTTAAGATC 420
 QY 1313 TCCGACCGGTACTGATACCGCGGATGCTGAACACCATGCTCTGCTTTACAAACGATG 1372
 DB 421 TCCGACCGGTACTGATACCGCGGATGCTGAACACCATGCTCTGCTTTACAAACGATG 480
 QY 1373 TTACTGCAACATGCGTGCAGATATTCCTGTCATGACAGAGCTGTATATCAACGCTCCG 1432

DB 481 TTACTGCAACATGCGTGCAGATATTCCTGTCATGACAGAGCTGTATATCAACGCTCCG 540
 QY 1433 GAATATCTATCATCAGGCTATGAAAGCGGACCCGTGATGATTTGGCTTCGACA 1492
 DB 541 GAATATCTATCATCAGGCTATGAAAGCGGACCCGTGATGATTTGGCTTCGACA 600
 QY 1493 CCACCAAGTTCATGTTCTCGGCTATGAGCAGGTTGTAACCTGCGTACCAACCACTGGG 1552
 DB 601 CCACCAAGTTCATGTTCTCGGCTATGAGCAGGTTGTAACCTGCGTACCAACCACTGGG 660
 QY 1553 CCGACGAAAAAGTCTTGAAGCGGCTATGAAAGCTTTGACAGCAAAAGTGTAGAG 1612
 DB 661 CCGACGAAAAAGTCTTGAAGCGGCTATGAAAGCTTTGACAGCAAAAGTGTAGAG 720
 QY 1613 GTAGACAGGAAAAATTTGATTAATGAGAAAGAGTTGAACCCGGGTCGGGGTTT 1672
 DB 721 GTAGACAGGAAAAATTTGATTAATGAGAAAGAGTTGAACCCGGGTCGGGGTTT 780
 QY 1673 ATTTCTCGTAGATCGACATTTATCCAGAACACAGACCGAGCTTGCAGAGCTGCATC 1732
 DB 781 ATTTCTCGTAGATCGACATTTATCCAGAACACAGACCGAGCTTGCAGAGCTGCATC 840
 QY 1733 TTCCATGCGTGTTCACCTTGAATGAAAGCACTTGGCCGCTGTGATACAGTGG 1792
 DB 841 TTCCATGCGTGTTCACCTTGAATGAAAGCACTTGGCCGCTGTGATACAGTGG 900
 QY 1793 TGAATTCGAAAGGTAGTGTGTAAGAAATACATCAGTCCGGGATACCGGAGAA 1852
 DB 901 TGAATTCGAAAGGTAGTGTGTAAGAAATACATCAGTCCGGGATACCGGAGAA 960
 QY 1853 CCGTGGATACCGCGTTACACACATAGCAGAGGCTTCTGTATGCAAAAGTTACTGCA 1912
 DB 961 CCGTGGATACCGCGTTACACACATAGCAGAGGCTTCTGTATGCAAAAGTTACTGCA 1020
 QY 1913 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTGACATGATCCGGCCACATATGCG 1972
 DB 1021 CAGTAAAGAGAAACGGGTATCGTTCCCTGTGTGACATGATCCGGCCACATATGCG 1080
 QY 1973 ATCAGATGATCGGTATATAGGCGCAGATATATACCTGACGATGACCAAAATCTTCG 2032
 DB 1081 ATCAGATGATCGGTATATAGGCGCAGATATATACCTGACGATGACCAAAATCTTCG 1140
 QY 2033 TTGGGCTCAACACAGCGAATTTGTCTTAACCGTATGAGCTTAACAGAAACCAACATGCG 2092
 DB 1141 TTGGGCTCAACACAGCGAATTTGTCTTAACCGTATGAGCTTAACAGAAACCAACATGCG 1200
 QY 2093 AAAATTAACCTTTCGCGATCATAGACACAGGTTCAACAAATGGGCTAAGAGCGCAAG 2152
 DB 1201 AAAATTAACCTTTCGCGATCATAGACACAGGTTCAACAAATGGGCTAAGAGCGCAAG 1260
 QY 2153 ATGATCTTGAATACAGAAAAATGCTGGGTACTAGAGAACCGAAGTATAGATATGCTGCT 2212
 DB 1261 ATGATCTTGAATACAGAAAAATGCTGGGTACTAGAGAACCGAAGTATAGATATGCTGCT 1320
 QY 2213 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTATGCGCCACTGGAACGAGACT 2272
 DB 1321 TGTGGGCGTTTCGCACTAAGAAAGTACATTCGTTTATGCGCCACTGGAACGAGACT 1380
 QY 2273 GCGTAAAGTCCCAAGCTCTTTTATGCGCTTTTCCATGTCGTCCGTAATGACGACTCTT 2332
 DB 1381 GCGTAAAGTCCCAAGCTCTTTTATGCGCTTTTCCATGTCGTCCGTAATGACGACTCTT 1440
 QY 2333 TGCCCATGTCGTGAGGACAGAAATTTGAATCTGGATTTGCAACCAAAAGAGAGAAAAAC 2392
 DB 1441 TGCCCATGTCGTGAGGACAGAAATTTGAATCTGGATTTGCAACCAAAAGAGAGAAAAAC 1500
 QY 2393 TGCTGACAGTCTCGAGAGAAATTAAGTCAATGAGAGCAAGGCTGCTTTGAGAGATGCTCAGG 2452
 DB 1501 TGCTGACAGTCTCGAGAGAAATTAAGTCAATGAGAGCAAGGCTGCTTTGAGAGATGCTCAGG 1560
 QY 2453 AGGAGGCAAGAGCGAGAAAGCTCGAGAAAGCACTTCCAGCAATTAAGTGGACAGCAAGGCA 2512

D 1561 AGAAGCGAAGCGGAGAACTCCGAGAACACTTCCACATTAGTGGACGACAAAGCA 1520
Q 2513 TCGAGCAGCGCGAGAAATTGTCTCGAGAGTGAAGGGCTCCAGCGCGACATCGAGCAG 2572
D 1621 TCGAGGACGCGCGAGAAATTGTCTCGAGAGTGAAGGGCTCCAGCGCGACATCGAGCAG 1680
Q 2573 CATTAGTTGAAACCCCGCGGCTCACTGAGATTAATCTCAAGCAATATGACCCGTATGA 2632
D 1681 CATTAGTTGAAACCCCGCGGCTCACTGAGATTAATCTCAAGCAATATGACCCGTATGA 1740
Q 2633 TCGGACAGTATATCTGTCTCGCAAACTCTGTGTAAGAAATGCAAACTCGACAG 2692
D 1741 TCGGACAGTATATCTGTCTCGCAAACTCTGTGTAAGAAATGCAAACTCGACAG 1800
Q 2693 CGGACCGGTAGCAGATCAGGTTAAGATCAATACACTCCGGAAGATCGAAGGTACG 2752
D 1801 CGGACCGGTAGCAGATCAGGTTAAGATCAATACACTCCGGAAGATCGAAGGTACG 1860
Q 2753 CGGTCCGACATACAGAGCTTAAAGTACTGATGCCAGAGAGGTCCGTACCATGGCCAG 2812
D 1861 CGGTCCGACATACAGAGCTTAAAGTACTGATGCCAGAGAGGTCCGTACCATGGCCAG 1920
Q 2813 AATTCTAGCAGTGAAGTGAAGCGCACGTTAGTGAAGCAAGAAAGAGTTGTGAAC 2872
D 1921 AATTCTAGCAGTGAAGTGAAGCGCACGTTAGTGAAGCAAGAAAGAGTTGTGAAC 1980
Q 2873 GCAAACTATACACATTGCCATGATGCCCCCGCAAGAAATACAGAGAGAGCATACA 2932
D 1981 GCAAACTATACACATTGCCATGATGCCCCCGCAAGAAATACAGAGAGAGCATACA 2040
Q 2933 AGGTACAAAGGCGAGACTTGCAGAAACAGATACGTTGTGACGTGGAACAAAGGTT 2992
D 2041 AGGTACAAAGGCGAGACTTGCAGAAACAGATACGTTGTGACGTGGAACAAAGGTT 2100
Q 2993 GCGTTAAGAGAAAGAGCCTCAGGCTCTGGTCTCTCGGAGAACTGACCAACCTCCCT 3052
D 2101 GCGTTAAGAGAAAGAGCCTCAGGCTCTGGTCTCTCGGAGAACTGACCAACCTCCCT 2160
Q 3053 ATCATGAGTACTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTACAGAGTGA 3112
D 2161 ATCATGAGTACTCTGAGAGGACTGAAGACCCGACCTGCGGTCCGTACAGAGTGA 2220
Q 3113 CATTAGAGTATAGGACACCGGGGTCGGGCAAGTACTATTTATTAAGTCAACTGTCA 3172
D 2221 CAATAGAGTATAGGACACCGGGGTCGGGCAAGTACTATTTATTAAGTCAACTGTCA 2280
Q 3173 CGGACAGAGTCTTTGTAACGACGCGAAGAAATTTGCGGAAATTGAGGCGGACG 3232
D 2281 CGGACAGAGTCTTTGTAACGACGCGAAGAAATTTGCGGAAATTGAGGCGGACG 2340
Q 3233 TGTCTAAGACTGAGGGGTATGCAATTAAGTGAAGACAGTAAATTCGGTTATGCTCAAG 3292
D 2341 TGTCTAAGACTGAGGGGTATGCAATTAAGTGAAGACAGTAAATTCGGTTATGCTCAAG 2400
Q 3293 GATGCCCAAAAGCGGTGAAGTGTCTGATGACGAAGCGTTCCGTGCAAGCGAGAG 3352
D 2401 GATGCCCAAAAGCGGTGAAGTGTCTGATGACGAAGCGTTCCGTGCAAGCGAGAG 2460
Q 3353 CACTACTGCTTGAATGCTATGCTGAGGCGCGCAAGAGGTAGTCTATGCGGAGAC 3412
D 2461 CACTACTGCTTGAATGCTATGCTGAGGCGCGCAAGAGGTAGTCTATGCGGAGAC 2520
Q 3413 CCAATGCAATGCGAATTTCTTAACATGATGCAACTTAAAGTACATTTCAATCACTGAAA 3472
D 2521 CCAATGCAATGCGAATTTCTTAACATGATGCAACTTAAAGTACATTTCAATCACTGAAA 2580
Q 3473 AAGAATATGACCAAGACATTTCTAAGATATCTCCCGCGTTGCAACAGCAGTTA 3532
D 2581 AAGAATATGACCAAGACATTTCTAAGATATCTCCCGCGTTGCAACAGCAGTTA 2640
Q 3533 CAGTATTTGATGACACTGATTAAGATGAAAGATGAAACCAAGAACCCGTCAGAA 3592
D 2641 CAGTATTTGATGACACTGATTAAGATGAAAGATGAAACCAAGAACCCGTCAGAA 2700

Q 3593 AGAATTTGAAATTCGATATTAAGGGGCCCAAAAGCCGAAGCCAGGGATATCATCTGA 3652
D 2701 AGAATTTGAAATTCGATATTAAGGGGCCCAAAAGCCGAAGCCAGGGATATCATCTGA 2760
Q 3653 CATGTTTCCGGGGGTGTTAAGCAATGCAATGCAATCCCGGACATGAAGTAATGA 3712
D 2761 CATGTTTCCGGGGGTGTTAAGCAATGCAATGCAATCCCGGACATGAAGTAATGA 2820
Q 3713 CAGCCGCGCTCACAGGGCTTAACGAGAAAGAGTATGCGCTCCGCAAAAAGTCA 3772
D 2821 CAGCCGCGCTCACAGGGCTTAACGAGAAAGAGTATGCGCTCCGCAAAAAGTCA 2880
Q 3773 ATGAAAACCACTGTAAGGATCACTGAGCATGTGAAGTGTGTCACCCGACTG 3832
D 2881 ATGAAAACCACTGTAAGGATCACTGAGCATGTGAAGTGTGTCACCCGACTG 2940
Q 3833 AGGACAGGCTAGTGTGGAACCTTGACAGGGGACCAAGATTAAGACCCACTACA 3892
D 2941 AGGACAGGCTAGTGTGGAACCTTGACAGGGGACCAAGATTAAGACCCACTACA 3000
Q 3893 TACCTAAGAAACCTTCAGGCTACTATAGAGGACTGGAAAGCTGAACAAAGGAATTA 3952
D 3001 TACCTAAGAAACCTTCAGGCTACTATAGAGGACTGGAAAGCTGAACAAAGGAATTA 3060
Q 3953 TTGCTCAATTAACAGCCCACTCCCGTCCATCCGTTCACTGCAAGACCAAGTTT 4012
D 3061 TTGCTCAATTAACAGCCCACTCCCGTCCATCCGTTCACTGCAAGACCAAGTTT 3120
Q 4013 GCTGGCGGAAGGATTTGGAACCGATCTAGCCACGCGGGTATCGTAACTTACCGGTGCG 4072
D 3121 GCTGGCGGAAGGATTTGGAACCGATCTAGCCACGCGGGTATCGTAACTTACCGGTGCG 3180
Q 4073 AGTGAAGCAACTGTTCCCAAGTTTCCGATGACAAACCAATTCGCGCATTTACGCT 4132
D 3181 AGTGAAGCAACTGTTCCCAAGTTTCCGATGACAAACCAATTCGCGCATTTACGCT 3240
Q 4133 TAGACGTAATTTGCAATTAAGTTTTCGCGATGACCTTGACAAAGCGGACTGTTTCTAAAC 4192
D 3241 TAGACGTAATTTGCAATTAAGTTTTCGCGATGACCTTGACAAAGCGGACTGTTTCTAAAC 3300
Q 4193 AAGGCAATCCCACTAAGTACATCCCGCGGATTCAGCGAGGCGCGATTAATGGGACA 4252
D 3301 AAGGCAATCCCACTAAGTACATCCCGCGGATTCAGCGAGGCGCGATTAATGGGACA 3360
Q 4253 ACAGCCCAAGAAACCGCAAGTATGGGTACATCAAGCATTCGCGCGCAACTCCCGTA 4312
D 3361 ACAGCCCAAGAAACCGCAAGTATGGGTACATCAAGCATTCGCGCGCAACTCCCGTA 3420
Q 4313 GATTTCCGGTGTCCAGTACTGAGGAGGCAACACTTGAATTTGACAGCGGAGAA 4372
D 3421 GATTTCCGGTGTCCAGTACTGAGGAGGCAACACTTGAATTTGACAGCGGAGAA 3480
Q 4373 CCAAGTATATCTGACAGCATTAACCTGTCGCGGTGAACCGCAATCTTCCCAAGCGCT 4432
D 3481 CCAAGTATATCTGACAGCATTAACCTGTCGCGGTGAACCGCAATCTTCCCAAGCGCT 3540
Q 4433 TAGTCCCGAGTACAGAGAGAAACAACCGCGCTCAAAAATTTCTTGAACAGTTCA 4492
D 3541 TAGTCCCGAGTACAGAGAGAAACAACCGCGCTCAAAAATTTCTTGAACAGTTCA 3600
Q 4493 AACACCACTCACTTGTGTATACAGAGAAAAATTAAGTCTCCCGTAAAGAAATCG 4552
D 3601 AACACCACTCACTTGTGTATACAGAGAAAAATTAAGTCTCCCGTAAAGAAATCG 3660
Q 4553 AATGATTCGCGCGGATTTGGCATTAAGCGGTCAGATTAAGAACTAAGAACTTGGGGT 4612
D 3661 AATGATTCGCGCGGATTTGGCATTAAGCGGTCAGATTAAGAACTAAGAACTTGGGGT 3720
Q 4613 TTCGCGCGAGGACGGTACGACTGTGTTATCAACTTGGAACTTAATACAGAAAC 4672
D 3721 TTCGCGCGAGGACGGTACGACTGTGTTATCAACTTGGAACTTAATACAGAAAC 3780

4673 ACCACTTTCAGCAGTGGAGAACCATGCGGACCTTTAAAAACCTTTCCGCTTCCGCCC 4732
4732 TGAATGTTTAACTCGAGGAGGACCGCTCGTGGAGTCTCTAAGGCTTACGCGGACCGCA 4792
3841 TGAATGCTTTAACCCAGAGAGGACCGCTCGTGGAGTCTCTAAGGCTTACGCGGACCGCA 3900
4793 ACAGTGAAGACGTAGTCAACGCTCTTCCAGAAAGTTTGTCAAGGCTTCTGACGCGAGAC 4852
3901 ACAGTGAAGACGTAGTCAACGCTCTTCCAGAAAGTTTGTCAAGGCTTCTGACGCGAGAC 3960
4853 CAGATGTTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGCAACATAGACAAACAGCC 4912
3961 CAGATGTTGTCTCAAGCAATACAGAAATGTACTGATTTTCCGCAACATAGACAAACAGCC 4020
4913 GTACACGGCAATTAACCCCGGACCATCTGAATTCGGGTGATTTGCTCCGTGTATAGAGGTA 4972
4021 GTACACGGCAATTAACCCCGGACCATCTGAATTCGGGTGATTTGCTCCGTGTATAGAGGTA 4080
4973 CAAGAGATGAGTTGAGCCGCGCTCATACCGCACCAAAAGGAGAAATTTCTGACT 5032
4081 CAAGAGATGAGTTGAGCCGCGCTCATACCGCACCAAAAGGAGAAATTTCTGACT 4140
5033 GTCAAGAGAGAGAGAGTTGTCAACGCGCAATCCGCTGGGTAGACAGCGGAGAGAGTCT 5092
4141 GTCAAGAGAGAGAGAGTTGTCAACGCGCAATCCGCTGGGTAGACAGCGGAGAGAGTCT 4200
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5153 CCGGAGAGATGACTGTGCTAGGAAAGAAAGTATCCAGCGGCTGGGCTGATTTCC 5212
4261 CCGGAGAGATGACTGTGCTAGGAAAGAAAGTATCCAGCGGCTGGGCTGATTTCC 4320
5213 GGAAGCAGCCAGAGAGAGAGCCCTTGAATTTCTTCAAAAACGCTTACCATGCACTGAG 5272
4321 GGAAGCAGCCAGAGAGAGAGCCCTTGAATTTCTTCAAAAACGCTTACCATGCACTGAG 4380
5273 ACTTAGTAATGAACATTAACATTAACATTAACATTAACATTAACATTAACATTAACATTA 5332
4381 ACTTAGTAATGAACATTAACATTAACATTAACATTAACATTAACATTAACATTAACATTA 4440
5333 ACGGAGCGGAGAAAGACCGGCTTGAAGTATCACTTACCTTGAACAACGCGCTAGACA 5392
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5393 GAACTGACGCGAGAGTAAACATTAATGCTGAGTAAAGAGTGAAGAGAAAGAAATCGACG 5452
4501 GAACTGACGCGAGAGTAAACATTAATGCTGAGTAAAGAGTGAAGAGAAAGAAATCGACG 4560
5453 CGGCACTTCCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATTCGACG 5512
4561 CGGCACTTCCAACTTAAGAGTCTGTAAACAGAGCTGAAGAGTGAAGATTCGACG 4620
5513 ATGAGTTAGTATGATTAATCAACAGAGTCTTGAAGAGAGAAAGGATTCAGTACTA 5572
4621 ATGAGTTAGTATGATTAATCAACAGAGTCTTGAAGAGAGAAAGGATTCAGTACTA 4680
5573 CAAGAAGAAATTTGATTCGACTTGAAGAGCAACAAATTCATCAAGCAGCAAAAGACA 5632
4681 CAAGAAGAAATTTGATTCGACTTGAAGAGCAACAAATTCATCAAGCAGCAAAAGACA 4740
5633 TGGCGGAGATTAAGGCTCTGTTCCCTTAATGACCAAGAAAGTATGAACAACCTGTGTGCT 5692
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5693 ACATATTTGGGTGAAGCATTGAAGAAATCCCGGAAATGCGCGGTGCAACATTAACCCGT 5752
4801 ACATATTTGGGTGAAGCATTGAAGAAATCCCGGAAATGCGCGGTGCAACATTAACCCGT 4860
5753 CGTCTAGCCGCGCAAAAGTTCGCTGCTTGTGATGTATGCAATGACGCGCAAGAAAGG 5812

4861 CGTCTAGCCGCGCAAAAGCTTCGCTGCTTGTGATGTATGCAATGACCGCAAGAAAGG 4920
5813 TCCACAGACTTAGAAGCAATTAAGTCAAAAGATTAAGTATGCTCTCCACCCCTTC 5872
4921 TCCACAGACTTAGAAGCAATTAAGTCAAAAGATTAAGTATGCTCTCCACCCCTTC 4980
5873 CTAAAGCAAAATTAAGATGTTTCAAGAGTTCAATGACGAAAGTATGCTCTGTTTATC 5932
4981 CTAAAGCAAAATTAAGATGTTTCAAGAGTTCAATGACGAAAGTATGCTCTGTTTATC 5040
5933 CGCAACTTCCCGGATTCGTTCCCGCGTAAGTACATAGAGTGCAGAACAGCTTACCG 5992
5041 CGCAACTTCCCGGATTCGTTCCCGCGTAAGTACATAGAGTGCAGAACAGCTTACCG 5100
5993 CTCTCTGTCAGACGAGCGGAGAGGCGCCGAAAGTTGAAGGACACGTCACCATCTACG 6052
5101 CTCTCTGTCAGACGAGCGGAGAGGCGCCGAAAGTTGAAGGACACGTCACCATCTACG 5160
6053 CTGATTAACACTCGCTTGAATGTCAAGACATCTCACTGATATGATGACAGTAGCGAAG 6112
5161 CTGATTAACACTCGCTTGAATGTCAAGACATCTCACTGATATGATGACAGTAGCGAAG 5220
6113 GCTCACTTTTGTGAGCTTTAGCGGATTCGAGCAACTTATTAATGATGACAGTTGCT 6172
5221 GCTCACTTTTGTGAGCTTTAGCGGATTCGAGCAACTTATTAATGATGACAGTTGCT 5280
6173 CGTCAGGACCTAGTCACTAGATAGTAGACGGAAGCAGAGTGTGTGCTGACGTTCC 6232
5281 CGTCAGGACCTAGTCACTAGATAGTAGACGGAAGCAGAGTGTGTGCTGACGTTCC 5340
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5341 ATGCGCTCAAGAGCTGCGCTGATTTCCACCGGCAAGCTTAAAGAAATGAGCCGCTCG 5400
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5401 CAGCGGCAAGAAAGAGCCCACTTCAACCGGCAAGCAATGAGTCTGATCCTTCACTCT 5460
6353 CTTTGGTGGGGTATCCATGTCCTGGATCAATTTTGAACGAGAGACGCGCCGACG 6412
5461 CTTTGGTGGGGTATCCATGTCCTGGATCAATTTTGAACGAGAGACGCGCCGACG 5520
6413 CAGCGGTAAACCCCTGCGCAACAGGCCCAACGAGTGTGCTATGCTTTTGGATCGTTT 6472
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6473 CCGACGAGAGATGATGAGCTGAGCGGCAAGATTAATGAGTCCGAACCCGCTCTGTTT 6532
5581 CCGACGAGAGATGATGAGCTGAGCGGCAAGATTAATGAGTCCGAACCCGCTCTGTTT 5640
6533 GATCATTTGAACCGGCGGAGAGTGAACATTAATATGTCCTCCGATCAGCCGATCTTTT 6592
5641 GATCATTTGAACCGGCGGAGAGTGAACATTAATATGTCCTCCGATCAGCCGATCTTTT 5700
6593 CACTACGCAAGCAGAGACGTAGACGAGAGCAGAGAGACTGAATTAATCTAAACCGGAG 6652
5701 CACTACGCAAGCAGAGACGTAGACGAGAGCAGAGAGACTGAATTAATCTAAACCGGAG 5760
6653 TAGGTGGGTATATATTTTGAACGAGCAACAGGCTCTGGCACTTGCAAAAGAGTCCGTT 6712
5761 TAGGTGGGTATATATTTTGAACGAGCAACAGGCTCTGGCACTTGCAAAAGAGTCCGTT 5820
6713 TGCAGAAACAGCTTACAGAACCGGACTTGAAGCGCAATGTCCTGGAAGAAATTCATGCCC 6772
5821 TGCAGAAACAGCTTACAGAACCGGACTTGAAGCGCAATGTCCTGGAAGAAATTCATGCCC 5880
6773 CGGTGCTGACACGTTCGAAAGAGAGCAACTCAACTCAGGTACCATGATGATGCGCACCG 6832
5881 CGGTGCTGACACGTTCGAAAGAGAGCAACTCAACTCAGGTACCATGATGATGCGCACCG 5940
6833 AAGCAACAAAGTATGATCAAGTCTCGTAAAGTGAAGAAATCAGAAAGCATTAACATG 6892

Db	5941	AAGCGAACAAGTAGGTACCAAGTCGTGTAAAGTAGAAAATCAGAAAAGCATAACCACTG	6000
Qy	6893	AGCGACTACTGTCAAGACTACGACTGTATTAACCTGCCACAGATCAGCAGATGCTATA	6952
Db	6001	AGCGACTACTGTCAAGACTACGACTGTATTAACCTGCCACAGATCAGCAGATGCTATA	6060
Qy	6953	AGATCACCTATCCGAAACCATTTGTACTCCAGTAGGTACCGGGCAACTACTCCGATCCAC	7012
Db	6061	AGATCACCTATCCGAAACCATTTGTACTCCAGTAGGTACCGGGCAACTACTCCGATCCAC	6120
Qy	7013	AGTTGCTGTAGCTGTCTGTAAACAATACTATCGATGAGAACTATCCGACAGTACATCTT	7072
Db	6121	AGTTGCTGTAGCTGTCTGTAAACAATACTATCGATGAGAACTATCCGACAGTACATCTT	6180
Qy	7073	ATCAGATTACTGACGAGTAGTCGATCTTATGGAATGTATGAGACGAGCACTGCGCATGCC	7132
Db	6181	ATCAGATTACTGACGAGTAGTCGATCTTATGGAATGTATGAGACGAGCACTGCGCATGCC	6240
Qy	7133	TGGATTACTGCAACCTTCTGCCCGCTAGCTTGAAGTTATCCGAAAAAATAGTAGATA	7192
Db	6241	TGGATTACTGCAACCTTCTGCCCGCTAGCTTGAAGTTATCCGAAAAAATAGTAGATA	6300
Qy	7193	GAGCCCCGAAATATCCGACGTGCGGTGTCCATCAGCGATGCAAGAACGCTACAAATGTGC	7252
Db	6301	GAGCCCCGAAATATCCGACGTGCGGTGTCCATCAGCGATGCAAGAACGCTACAAATGTGC	6360
Qy	7253	TCATTTGCCCGCACTPAAAGAAATTGCCAGCTCAGCGAGTCGCGTAACCTGCCACACTGG	7312
Db	6361	TCATTTGCCCGCACTPAAAGAAATTGCCAGCTCAGCGAGTCGCGTAACCTGCCACACTGG	6420
Qy	7313	ACTCAGCGCACTTCAATGTGCAATGCTTGGAAAATATGATGTATGACGAGATTTGGG	7372
Db	6421	ACTCAGCGCACTTCAATGTGCAATGCTTGGAAAATATGATGTATGACGAGATTTGGG	6480
Qy	7373	AGGAGTTGCGTCGGAAGCCAAATTAGAAATACACTGAGTTTGTCAACGCAATGTAGCTA	7432
Db	6481	AGGAGTTGCGTCGGAAGCCAAATTAGAAATATGATGTATGACGAGATTTGTCAACGCAATGTAGCTA	6540
Qy	7433	GACTGAAAGGCCCTPAGGCGCGCCGCACTATTTGCCAAGAAGCTATATTGGTCCCATTTGC	7492
Db	6541	GACTGAAAGGCCCTPAGGCGCGCCGCACTATTTGCCAAGAAGCTATATTGGTCCCATTTGC	6600
Qy	7493	AAGAAGTGCCTATGGAATGTGATTTGCAATGGAATGAAAGAGAGTGAAGTTTACACAG	7552
Db	6601	AAGAAGTGCCTATGGAATGTGATTTGCAATGGAATGAAAGAGAGTGAAGTTTACACAG	6660
Qy	7553	GCACGAAACACACAGAGAAAGAACCGGAAGTACAGTGTATCAACGCGCAAAACCCCTGG	7612
Db	6661	GCACGAAACACACAGAGAAAGAACCGGAAGTACAGTGTATCAACGCGCAAAACCCCTGG	6720
Qy	7613	CGACTGCTTACTTATGCGGGATTCAACGGGAATTAGTGCCTGAGGCTTACGGCGCTTTGC	7672
Db	6721	CGACTGCTTACTTATGCGGGATTCAACGGGAATTAGTGCCTGAGGCTTACGGCGCTTTGC	6780
Qy	7673	TTCCAAACATATCACACGCTTTTTCACATGTGCGGGAGGATTTTGAATGCAATCATACAG	7732
Db	6781	TTCCAAACATATCACACGCTTTTTCACATGTGCGGGAGGATTTTGAATGCAATCATACAG	6840
Qy	7733	AACACTTCACAAAGCGACCCCGGTCTGAGACGGAATATCGCATCTTGCACAAAAGCC	7792
Db	6841	AACACTTCACAAAGCGACCCCGGTCTGAGACGGAATATCGCATCTTGCACAAAAGCC	6900
Qy	7793	AAGACGACGCTATGGCGTTTAAACGGGTCTGATGATCTTGGAGAGACTGGGTGTGATCAAC	7852
Db	6901	AAGACGACGCTATGGCGTTTAAACGGGTCTGATGATCTTGGAGAGACTGGGTGTGATCAAC	6960
Qy	7853	CACATCTCGACTTGTATCGAGTGGCGCTTTGGAGAAATATCATCCACCATCTACCTACGG	7912
Db	6961	CACATCTCGACTTGTATCGAGTGGCGCTTTGGAGAAATATCATCCACCATCTACCTACGG	7020
Qy	7913	GTACTCGTTTAAATTCGGGGCGATGTAGAAATCCGGAATGTCCTCACTTTTGTCA	7972
Db	7021	GTACTCGTTTAAATTCGGGGCGATGTAGAAATCCGGAATGTCCTCACTTTTGTCA	7080

QY	7973	ACACAGTTTGAATGATGCTTATGCGCAGCAGAGACTACGAAAGACGGCTTAAACGTC	80322
Db	7081	ACACAGTTTGAATGATGCTTATGCGCAGCAGAGACTACGAAAGACGGCTTAAACGTC	71404
QY	8033	GATGTGACGGCTTCATTGGCGACGACAACATCATACATGAGTAGTATCTGACAAGAAA	80929
Db	7141	GATGTGACGGCTTCATTGGCGACGACAACATCATACATGAGTAGTATCTGACAAGAAA	72000
QY	8093	TGGCTGAGAGGTGCGCCACTGGCTCAACATGAGGTTAAGATCATGACGCAGTCA	81523
Db	7201	TGGCTGAGAGGTGCGCCACTGGCTCAACATGAGGTTAAGATCATGACGCAGTCA	72606
QY	8153	GTGAGAACCAACCTTATCTGCGCGCGGATTTATCTTGCAAGATTCGGTTACTCCAC	82122
Db	7261	GTGAGAACCAACCTTATCTGCGCGCGGATTTATCTTGCAAGATTCGGTTACTCCAC	73202
QY	8213	CGTCCCGCGTGGCGGATCCCCGTGAAAAGCGTGTTAAGTTGGGTTAAACCGCTCCAC	82727
Db	7321	CGTCCCGCGTGGCGGATCCCCGTGAAAAGCGTGTTAAGTTGGGTTAAACCGCTCCAC	73800
QY	8273	ACGACGAGCAAGACGAAGAACAAGACGCGCTCTGCTAATGTAAGAAACAAAGCGTGTT	83322
Db	7381	ACGACGAGCAAGACGAAGAACAAGACGCGCTCTGCTAATGTAAGAAACAAAGCGTGTT	74400
QY	8333	GAGTAGGTATTAACGAGCACTTTAGCACTGGCCCGGAGACACCCGGTATGAGTAAACATA	83922
Db	7441	GAGTAGGTATTAACGAGCACTTTAGCACTGGCCCGGAGACACCCGGTATGAGTAAACATA	75000
QY	8393	TTACACCTGTCTCACTGCGCATTTGGAACCTTTGGCCGAGACAAAGAGACATCTCAAGCA	84522
Db	7501	TTACACCTGTCTCACTGCGCATTTGGAACCTTTGGCCGAGACAAAGAGACATCTCAAGCA	75600
QY	8453	TCAGAGGGGAAATPAAGCATCTCTACGSGTCTCTAATATGTCAGCATAGTACATTT	85122
Db	7561	TCAGAGGGGAAATPAAGCATCTCTACGSGTCTCTAATATGTCAGCATAGTACATTT	76200
QY	8513	CTGACTAATATCAACACACCAACCT	8539
Db	7621	CTGACTAATATCAACACACCAACCT	7647

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